

FIGURE 1

CCAATGCCCGGTGCGGTGGTGCAGGGCTCGGGCTAGTC**ATGGCGTCCCCGTCGGAGAC**
TGCAGACTAAACCAGTCATTACTGTTCAAGAGCGTCTGCTAATCTACACTTTATTT
TGGATCACTGGCGTTACCTCTTGCAAGTGGCATTTGGCAAGGTGAGCCTGGAGAATT
CTTTCTCTTTAAATGAGAAGGCCACCAATGTCCTCGTGCCTATTGCTACTGGTACCG
TCATTATTCTTTGGCACCTTGGTTGCTACCTGCGAGCTCTGCATGGATGCTA
AAACTGTATGCAATGTTCTGACTCTCGTTTTGGTGAACACTGGTCGCTGCCATCGTAGG
ATTGTTTCAGACATGAGATTAAGAACAGCTTAAAGAATAATTATGAGAAGGCTTGAAGC
AGTATAACTCTACAGGAGATTATAGAACGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT
TGGTGTGGTGCACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAGGATT
TCCTAAGAGTTGCTGTAACCTGAAGATTGACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTTGTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGGAG
ATTTCCCTTGGAGTTGCTGCTTCCAACGTGGAAATCTTCTCGCCTACTGCCWCTCTCG
TGCCATAACAAATAACCAGTATGAGATAGTG**TAA**CCCAATGTATCTGTTGGCCTATCCTCT
CTACCTTAAGGACATTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAAGT
ACAACACTACTTACTGATAGACCAAAAAACTACACCCAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT
TCAATCAAGATGTATGTTGCTATGTTCTAAGTCCACCTTCTATCCATTCAATGTTAGATCG
TTGAAACCCGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAATGAAGT

FIGURE 2

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><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGKVSLENYFSLLNEKATNVPF
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDTNYYSEKGFPKSCCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRAlTNNQYEIV
```

Important features of the protein:

Signal peptide:

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVGVLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

FIGURE 5

GGCACGAGGCCTGTCACCCGGGGCGTGGGAGTGAGGTACCAAGATTCAAGCCCATTGGCC
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCCGTTCTAACGGACTG
CAAGATGGAGGAAGGCGGGAACCTAGGAGGCTGATTAAGATGGTCATCTACTGGTCTTGT
CAGGTGCCTGGGCATGCAAATGTGGGTGACCTCGTCTCAGGCTTCTGCTTTCCGAAGC
CTTCCCCGACATACCTCGGACTAGTGCAAGAGCAAACCTCTCCCCCTACTTCCACATCTC
CATGGGCTGTGCCCTCATCACCTCTGCATCTGGCTTCACAGCATGCTGGCTCAGCTCA
CATTCTGGGAGGCCAGCCAGCTTACCTGCTGTTCTGAGCCTTACGCTGGCCACTGTCAAC
GCCCGCTGGCTGGAACCCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGGTGGGGAGGTACCAAGGCAGGCCAGGGTCCCGATCCCTACCGCAGCTCC
GAGAGAAGGACCCAAGTACAGTGCTCTCGCCAGAATTCTCGTACCATGGCTGTCC
TCTCTTGCAATCTGGGCTGCGTCTGAGCAATGGGCTCTGCTCTCGCTGGCCTGCCCTGGA
AATAAGGAGCCTCTAGCATGGGCCCTGCATAAATGCTTCTTCAGAAATGAAAAAAA
AAAAAAAAAAAA

FIGURE 6

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107
<subunit 1 of 1, 231 aa, 1 stop
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GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQTVEKER
GLGGEVPGSHQGPDPYRQLREKDPKYSALRNFFRYHGLSSLNLGCVLSNGLCLAGLALEIRSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

AATTCA GATTTAAGCCCATTCTGCA GTGGAATTCATGA ACTAGCAAGAGGGACACC ATCTT
 CTTGTATTATA CAAGAAAGGAGTGTA CCTATCACACACAGGGGGAAA **ATG**CTTTGGGT
 GCTAGGCCTCCTAATCCTCTGTTCTGTGGACTCGTAAAGGAAA ACTAAAGATTGAAG
 ACATCACTGATAAGTACATTTTATCAGTGGATGTGACTCGGGCTTGGAAACTTGGCAGCC
 AGAACCTTTGATAAAAAGGGATTCTATGTAATCGCTGCCGTCTGACTGAATCAGGATCAAC
 AGCTTTAAAGGCAGAACCTCAGAGAGACTCGTACTGTGTTCTGGATGTGACCGACCCAG
 AGAACATGTCAGAGGACTGCCAGTGGGTGAAGAACCAAGTGGGGAGAAAGGTCTGGGT
 CTGATCAATAATGCTGGTGTCCCGCGCTGCTGGCTCCACTGACTGGCTGACACTAGAGGA
 CTACAGAGAACCTATTGAAGTGAACCTGTTGGACTCATCAGTGTGACACTAAATATGCTTC
 CTTGGTCAAGAACGCTCAAGGGAGAGTTAATGTCCTCAGTGGTGGAGGTGCCCTTGCA
 ATCGTTGGAGGGGCTATACTCCATCCAATATGCA GTGGAAGGTTCAATGACAGCTTAAG
 ACAGGGACATGAAAGCTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAACAA
 ACTTGGCAGATCCAGTAAGGTAATTGAAAAAAACTCGCCATTGGGAGCAGCTGTCTCCA
 GACATCAAACAACAATATGGAGAAGGTTACATTGAAAAAAAGTCTAGACAAACTGAAAGGCAA
 TAAATCCTATGTGAACATGGACCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA
 GTCTCTCCCTAAGACTCATTATGCCGTGGAAAAGATGCCAAATTCTGGATACCTCTG
 TCTCACATGCCAGCAGCTTCAAGACTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
 TCCCAGGCAGTG**TGA**CTCAGCTAACCAAATGTCCTCCAGGCTATGAAATTGCCGAT
 TTCAAGAACACATCCTTCAACCCATTCTTATGCTCCAACCTGGACTCATTTAGA
 TCGTGCTTATTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGCCCTG
 CTCAAGTTCTTGTGAAAAGGGCTGGAATGGTACATCACATAGGCAAGTCTGCCCTG
 ATTTAGGCTTGCCTGCTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCATTCAAATG
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 AAGTATCATCTTATCTAAATATTAAGATAAGTCAACCCAAAAAA
 AAAAAAAAAAAAAAA

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
><subunit 1 of 1, 319 aa, 1 stop
>**MW:** 35227, **pI:** 8.97, **NX(S/T):** 3
MLFWVLGLLILCGFLWTRKGKLKIEDITDKYIFITGCDSGFGNIAARTFDKKGFHVIACLT
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LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSSLRRDMKAFCGVHVSCIEPGLFKTNLADPVKIEKKLAIWEQLSPDIKQQYGE
KLKGKNSYVNMDLSPVVECMDHALTSLFPKTHYAAGKD
AKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 9

GCGGGCTTTGACGGCGTGC~~G~~**A**TGGCTGCCGTGGAGGGCAGGAGAACGGAGCTCTCGGTT
 CCTCTCATGCGACTTCCGTACGCCGCACTGGGCGGGCCCCCTGGGCCGTCGCCACCACT
 GTAGTCATGTA~~CCC~~ACCGCCGCCGCCCTCATGGGACTTCATCTCGGTGACGCTGAG
 CTTTGGCGAGAGCTATGACAACACAAAGGATTGGCGGCCGCGCTGTGCTGGAGGAATGGGA
 AGCAACTGTGAGATTGAGCGGAATATGATTCTCTTCTTCTGCTTCTGCTTTCTGCTTTCTGT
 GGACTCTCTCTCATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTCAAGCTAGAGGA
 AGAGCAGAAAGATGAGGCCAGAAATTGCTGGTTAACACAGCAAATCCACCCGTTACACAG
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 AGACACATCCAGGGGACCTCACCTCAGGATTAGACCCCCAAGCCAAGACCTGAAGGA
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 CTCCCTCAAGAAGAGCAGAAGTGCCCACCAAGCCTCCCTGCCACGGCCAGGACACAGGG
 CACACAGTGCATCTGAACATCCGCAAGGGCTGATTGAGCTTCCATGCTGAGTGG
 AAGGATA~~CCC~~AAAGTTCGATGGG~~CC~~ATGAGCTGAGCTGAGCTGAGGCTTCCATG
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 GAGGAAAGAATTGAGGAAGCCAGGAAGTGGGTGTCGAAGAAGTTACACTTGAAGGAGC
 TGGACGTCACCTGTTGGAGAGCACGATCCGCATCTGGGGGGCTCTGAGTGCCTACCAC
 CTCGCTGGGGCACGAGCTCTCTCTGGAAAGACTGGAGATTGGAAATCGGCTAATGGCT
 CTTCAGAACACCATCCAAGATTCCCTACTCGGATGTGAACATCGGTACTGGAGTGGCCACC
 CGCCCAAGCTGGACCCAGCAGCTGGCCAGGGTACGGCAGCATTCAGCTGGAGTTCCGG
 GAGCTCTCCCGTCTCACAGGGATAAGAAGTTTCAGGAGGAGCTGGAGACAGCA
 CATCCACGGCTGTCGGAAAGAAGATGGGCTGGTGCCTGTTCATCAATACCCACAGTG
 GCCTCTTCACCCACCTGGCGTATTCACTGGCCAGGGCAGCAGCTACTATGAGTAC
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 AGGATCATGAGGGTGTCAAGACGCACTCTGCGCAGACTCAGGCCAGTAAGCTCACCTTG
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 GGGACGCTGCTCTGGCTCACACGGCTGCCAGGCCACATGGAGCTGGCCAGGA
 GCTCATGGAGACTTGTACCATGAA~~CC~~GGCAGATGGAGACGGGGCTGAGTCCCGAGATCG
 TGCACTTCAACCTTACCCCCAGCCGGCGTGGGAGCTGGAGGTCAAGCCAGCAGACAGG
 CACAACCTGTCGGCCAGAGACCTGGAGAGCTGTTCTACCTGTACCGCGTCAACAGGGGA
 CGCGAACATACAGGACTGGGCTGGAGATTCTGAGAGCTTCAGCCATTACACGGTCC
 CCTCTGGTGTGATTCTCCATCAAAATGTCAGGATCTCAGAAGCCGAGCTAGGGAC
 AAGATGGAGACTTCTTCTGGGGAGACGCTCAAGTATCTGTTCTCTCCGATGA
 CCCAACCTGCTCGCCAGCTGAGCCTACGTGTTCAACACCGAAGGCCACCCCTGCTATCT
 GGACCCCTGCC**TAGGGTGTGATGGCTGTTG**GGAGCTTCGGGTGGCAGAGGACCTTG
 CTGGGTCTGTCATTTCAAGGGCCACGTAGCACCGCAACGCCAAGTGGCCAGGCT
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FIGURE 10

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529
><subunit 1 of 1, 699 aa, 1 stop
><MW: 79553, pI: 7.83, NX(S/T): 0
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IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIGRGPPHLQIRPPSQDLKDGTQEETAT
KRQEAPVDPDPRPEGDPQRTVISWRGAVIEPEQGTELPSSRAEVPTKPPPARTQGTPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVDVNLFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRRLMPAFRTPSKI
FYSDVNIGTGVAHPPRWTSDSTVAEVTSIQLEFRELSRLTGDKKFQEAVEKVITQHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTL GARADSYYEYLKQWIQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLT FVGELAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MN RQMETGLSPEIVHFNLYPQPGRDVEVKPADRHNLRLPETVESLFYLYRVTGDRKYQDWG
WEILQSF SRFTRVPSSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFL FSDDPNLLSLD
AYVFNTEAHPLPIWTPA
```

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

FIGURE 11

GGCCGCCGCTAGGCCGGAGGCCGGCGCCGGCTGCAGGCCCTGCCCATGCC
CGCCTCTCCGCACGATGTCCCCCTCGGGAGGAAGCGCGCAGCTGCCCTGGGAGGACGGC
AGGTCCGGTTGCTCTCCGGCGCCTCCCTCGGAAGTGTTCGTCTCCACCTGTTCTGTTGGC
CTGCCCTCTGCTGGCTTCTCTCCACTCTGGCTCAGCTCAGCTGCTCTGGGAGCTGG
CCGGGCAGTCAGGGACAAGGGCAGGAGACCTCGGGCCCTCCCGTGCTGCCCTCCCCCAGAG
CGGCCCCCTGAGCACTGGGAAGAAGACCATCCTGGGGCCCCCACCGCTGGCAGTGCTGGT
GCCCTTCCGCAACGCTTCGAGGAGCTCTGGTCTTCGTGCCCCACATGCCCGCTTCTGAA
GCAGGAAGAAGATCCGCACCACATCTACGTGCTAACAGCTGGACACTTCAGGTCAAC
CGGGCAGCGCTCATCAACGTGGCTTCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTCTGAGGCTGGC
CCTTCCACGTGGCTCCCCGGAGCTCACCCCTCTACCAACTACAAGACCTATGTCGGCGG
ATCCTGCTGCTCTCCAAGCAGCACTACCGCTGTGCAATGGGATGTCCAACGCTCTGGGG
CTGGGGCCCGAGGAGCACGAGTCTACCGCGCATTAAAGGGAGCTGGCTCCAGCTTTCC
GCCCTCGGAATCACAACGGTACAAGACATTCCCACCTGATGACCCAGCCTGGCGG
AAAGGGGACAGAAGCGCATCGCACCTAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG
AGGCTGAACACTGTGAAGTACCATGTGGCTTCCGCACTGCCCTGTCTGTGGGGGGGG
CTGCACTGTCTCAACATCATGTGGACTGTGACAAGACGCCACACCTGGTGCACATT
ACGCTGAGCTGGATGGACAGTGAGGAAGGCTGTACCTACAGGCCATTGCTCAGGCTCAGGA
CAAGGCCCTAGGTGCTGGGCCAGCTCTGACAGGATGTGGAGTGGCAGGACCAAGACAGCA
AGCTACGCAATTGCAAGCACCCGGCGCAAGGCAGGCTGGGCTGGGCCAGGACACGTGGG
GTGCCCTGGGAGCCTGCTTGCATGCACAGTGTACAGAGAGAGGCTGGGGTGTCTGCTGG
GGACCCCCCTGCCTTCTGCTCACCTACTCTGACCTCCTCACGTGCCAGGCCCTGGGG
TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCTACTCTGACCTCCTCACGTGCC
AGGCCCTGTGGTAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 12

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531
><subunit 1 of 1, 327 aa, 1 stop
><MW: 37406, pI: 9.30, NX(S/T): 1
MFPSRRKAAQLPWEDGRSGGLPRKCSVFHLFVACLSLGFFSLLWLQLSCSGDVARAVR
GQQQETSGPPRACPPEPPPHEWEEDASWGPHRLAVLVPFRERFEELLVFVPHMRRFLSRKKI
RHIIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDV DLLPLNEELDYGFPEAGPFHVA
SPELHPLYHYKTYVGGILLSKQHYRLCNGMSNRFWGWGREDDDEFYRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDQKRIAAQKQEKFVVDREGGLNTVKYHVASRTALSVGGA PCTVL
NIMLD CDTATPWCTFS
```

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 13

CAATGTTGCCCTATCCACCTCCCCAAGCCCCTTACCTATGGCTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTAAAGGCTCATGCTGGAGTGGGACTGGTCGGTGCCCAGAAAGTCT
CTTCTGCCACTGACGCCCATCAGGGATTGGGCCTTCTTCCCCCTCCCTTGTGTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGAAGGGGAGAAAGT
GGGGGATGGTAAGAAAGCTGGAGATAGGAAACAGAAGAGGGTAGTGGGTGGGCTAGGGG
GCTGCCTTATTAAAGTGGTTATGATTCTTATACTAATTATAAAAGATATAAGGC
CCTGTTCATTAAGAAATTGTTCCCTCCCTGTGTTCAATGTTGTAAGATTGTTCTGTGT
AAATATGTCTTATAATAAACAGTTAAAAGCTGAAAAAAAAAAAAAAA

FIGURE 14

```
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<subunit 1 of 1, 73 aa, 1 stop
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PRGEGEKVGDG
```

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

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FIGURE 15

GGGACCCATGCGGCCGTACCCCCGGCTCCCTAGAGGCCAGCGCAGCGGACAAAG
 GAGCATGTCCGCAGGGGAAAGGCCGCTCTCCGGGCCATAAGGCTCCGGTCCCGCTGG
 GCCCCCGCCCGCTCTGCCGCCGGCTCAGGGGGCGCTAGGCCAGTCCGCCGCG
 CTCGCCCCGAGGCCCGCCGAGCAGTCAGGCCACCCGGACGCCGGGGCGCG
 GCGCCGCGCTGTTGCTGCCGTCTCGCTGTTAGCGCTGCTCGCCTGCTGGGAGGCCGGCG
 GCGGCCGGCCGGCGCCGGCTGCCGCCGCAAGCGAGCATGGGCGGCCCGAGGGGCTGGC
 AGGGCGCGGGCGCCGCCGGGAAGGGCAAGGTGGTGTGAGCAGCCTGAAACTCGCCAGGTCC
 GCCCCCAGATACTCTGCCAACCGCACGGTACCCCTGATTCTGAGTAACAATAAGATATCCG
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 CTATTAGTAGTATAGATCAGGGCTCTCTGGGAGCTGTCATCTCTAAAAGATTGGATCT
 GACAAACAATCGAATAGGATGTCATGAGCAGACATATTCTGAGGACTCACCACATCTGGTTC
 GGCTAAACCTTCGGGAATTGTTCTCATTATCTCAAGGAATTTCGATTATCTTGCG
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 GCATCGCTGGTAAAGGAGAAAGAACATCACGGTACCGGGATACCCAGGTGTTTACCTAAGT
 CACTCGAGGCCAACACTACAGCGTGAACCGAGCTGTTGACATCGGACCCCGCTT
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 TCTCTTCCAGTGCATGGCTCATATTGATCAGGACATGCCAACGTTGTTGAGGAGACAGCCT
 GGAAGAATAGTTGAAACCGATGAATCCAAGGATTTTGTGAAAAAGAACATGATTCACAAC
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 AGAGTTCTGCAAGCTACTGCTCCCTCAGAGGGCTGGTAAACAAACAAAGGTGACTTCAGATGG
 CCCAGAACATGGCAGGCAATTACTGCATATCTGCACTGTTGACTGCCAACCCATGGCAGTGG
 GATATATCCGGAAACCCACAGGTGAGGAAAAGCTGGCGCAGATGTGATAGGGTGGCT
 TTGGCAGATGATGATTATCTGCTGTCAGTATGCCAATGATGTCAGTGGATCTTCTTAT
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 GACATTGCAAGTAACATCATGTTGGCTGTGATGAACTGTCCTGTGGCTGCCAGAGGAAAGC
 TAAAGCCTGCACTGAGGATTGTCAGTGTCTCAGCGCATTGCTACCCGGCTAGCCGGTG
 GAGCTCACGTTTACCAATTACCCCAATTGCTCTGGAAAGCTTATGTCATCACAGTCT
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 AAAGATTTTTTGGCAGGAAAGATAGTATTGTTCTGTTACTGTTTAAAGAAAAGTATTCA
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 ATCAAAATTTGGCAGAAAACACAAATGTCATATCTTTTTAAAAAGTATTCA
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 GACTACACTGTATTGAGCAAATAGAGGAGGCAAACTCCAGCACCTAATGAAACACATT
 TTTTCACTGCTGCTTGTGGCACTGTGTAATTGTTCTGCGGTTTTAACTCAG
 TACTTTATTCTGCTTGTGCTTAATATCACAAACAAATATTCCAGTCATTAAATGGC
 TGCTAATAACTGATCCACAGGTGTTAGGTCTGGTTAGTGTGAGCACTCAATAAATA
 TTGAATGAATGAACGAAAAAAAAAAAAAA

FIGURE 16

MEPPGRRRGRAQPPPLLPLSLLALLALLGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
 VVCSSLELAQVLPPDTLPNRTVTLILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
 FWGLSSLKRLLDTNNRIGCLNADIFRGLTNLVRNLSGNLFSSLSQGTFDYLASLRSLEFQT
 EYLLCDCNILWMHRWVKEKNITVRDTRCVPKSLQAQPVTGVKQELLTCDPPELPSFYMTP
 SHRQVVFEGDLSLPFQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIHNCSLIASALT
 ISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRWPTLAGITA
 YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDYSRCQYANDVTRVLYMFNQMPLNL
 TNAVATARQLLAYTVEAANFSKMDVIFVAEMIEKFGRFTKEEKSKELGDVMDIASNIMLA
 DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
 VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
433-437, 453-457, 592-596**N-myristylation site.**amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
384-390, 403-409, 554-560

FIGURE 17

GCCTGGGGATGCTAGGAGCTCGAAGGTGGTCTGGGCCTCTGGTGTGCTGACGGCGGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCAATTGGAAAAAGAAAACATTGCTTTGGAGAACAGATTAA
TTTGACTGAGCAACTGAACAGAAAAGAGAGAACAGATGTTATGGCAAAAGGATCTAAAAAA
TCATGACTTGAATGTGAATATCTGTTGGACAGACAACACGAGTTGTGTGTGTTGATCA
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTGGTCACTGTCCTTAAACTGATCA
AATAAAGGACAGTGGTCATAAAGTTACTGCTTCAGGGTCCCTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTTGGAGAGTGTCTGGGTGATCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGTAGGGTTACTGAGAACGACTGCCAGCTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTGTGATCAGTGGCATGATGACGAAGCCACCGAGAAC
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACCTCTGTGACGGCAATCC

FIGURE 18

MSRSSKVVLGLSVLLTAATVAGVHVKKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGQSQKS

Signal peptide:

amino acids 1-21

(a)
(b)
(c)
(d)
(e)
(f)
(g)
(h)
(i)
(j)
(k)
(l)
(m)
(n)
(o)
(p)
(q)
(r)

FIGURE 19

CTGTCGTCTTGCTTCAGCCGCAGTCGCCACTGGCTGCCCTGAGGTGCTCTTACAGCCTGTT
 CAAGTGTGGCTTAATCCGTCCTCACCAACAGATCTTCTCGTGGATTCTCTGCTAAAGACC
 GCTGCC**ATGCC**AGTGA~~CG~~TAACCCGCACCACCATACAACCACACGACGT~~C~~ATCTCGGG
 CCTGGGGTCCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAGCCCTGGTCTCTTCGC
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGTGGTGTAGCGTGGCGCCTGGAC
 GGGTCCATGGCAACTGGTCCATGTTACCTGGTGTCTGCTTCTCGTGGCCTGACCTGATCA
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCCTTCCCTGTCTGGCGCAACTTCCCC
 ATCACCTCCGCTGCTATGCGGCCCTCTCTGCCTCTCGGCCATCATCTACCCCCAACAC
 CTATGTCCAGTCCCTGTCACGGCGTTCGCGGGACCACGCCATGCCGCCACCTCTTCT
 CCTGCATCGGTGTGTCCTACGCCACCGAAGTGGCTGGACCCGGCCGGCCGGCGAG
 ATCACTGGCTATATGGCACCGTACCCGGGTGCTGAAGGTGCTGGAGACCTTCGTTGCGCTG
 CATCATCTTCGCGTTCATCAGCGACCCAACCTGTACCAAGCACCAGCCGGCCCTGGAGTGGT
 GCGTGGCGGTGTACGCCATGTCCTCATCTAGCGGCCATGCCATCTGCTGAACCTGGGG
 GAGTGCACCAACGTCTACCCATCCCCTCCCCAGCTCTGTGCGGGCTGGCCTGCTGTC
 TGTCTCCTCATGCCACCGCCCTGTCTCTGGCCCTCTACCAAGTCGATGAGAAGTATG
 GCGGCCAGCCTCGGCCTCGAGAGATGTAAGCTGCAGCGCAGCCATGCCACTACGTGTG
 GCCTGGGACCGCCGACTGGTGTGCCATCTGACGGCCATCAACCTACTGGGTATGTGGC
 TGACCTGGTGCACTCTGCCACCTGGTTTGTCAAGGTC**TAA**GACTCTCCAAGAGGCTCC
 CGTTCCTCTCCAACCTTTGTCTTCTGCCCCAGTTCTTATGGAGTACTCTTCCC
 TCCGCCCTTCTCTGTCTTCTCTTCTCTGCCACCTTTCTTCTCTTCCC
 CAATTCTTGCACCTAACCAAGTCTGGATGCATCTCTCTCTCTCTCTGCTGTC
 TTCTCTCTGTGTTGTTGTTGCCACATCCTGTTCTACCCCTGAGCTGTTCTCTTCTTCTTCTTCT
 CTTCT
 TGCAGTGGTGCAGTCTCAGCTACTGCACCCCCCGCCCTGGGTCAAGCGATTCTCC
 CCCAGCCTCCAAGTAGCTGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTCTTCT
 TTCCACTCTCTCTCTCTCATCTCTCTCTGGGTTGCCCTGCGCTTCTTATCTGCCGT
 TTTGCAAGCACCTCTCTCTGTCCTGGAGCCCTGAGACTCTCTCTCTCTCTCTCT
 CCCACCTCAAAGGTGCTGAGCTCACATCACACCCCTGAGCCGTCATGCCACAGCCCC
 CCAAGGGCCCCATTGCCAAAGCATGCCCTGCCACCCCTGCGTGTGCCCTAGTCAGTGTAC
 GTGTGTGTGTGTGTGTTGGGGGGTGGGGGGTGGGTAGCTGGGATTGGCCCTCTTCT
 CCCAGTGGAGGAAGGTGTCAGTGTACTTCCCTTAAATTAAAAACATATATATATAT
 ATTGGAGGTCACTTCAATTCCAAATGGGGGGAGGCATTAAGCACGCCCTGGTCCCTAGG
 CCCCGCCTGGCACTCAGCCTGCCAGAGATTGGCTCCAGAAATTGGCAGGCTTACAGAACAC
 CCACTGCCCTAGAGGCCATCTTAAAGGAAGCAGGGCTGGATGCCCTTACCCAACTATTCT
 CTGTGGTATGAAAAAG

FIGURE 20

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTTRTTTTSSSGLGSPMIVGSPRALTQPLGLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIYPTTY
VQFLSHGRSRDHAIATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQPALEWCVAVYAIICFILAIAIALLNLECTNVLPPIPFPFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYVCAWDRRILAVAILTAINLLAYVAD
LVHSAHLVFVKV
```

Important features:

Transmembrane domains:

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

FIGURE 21

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSFPSHPKVHMDPNYCHPSTSLHLCS
LAWSFTRLLHHPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESAFSSY
SDLSEGEQEAFRAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAAGGMDTDAGQLPLG
PHLQDLFTGHRFSPVRQGSVEPESDCSQTVPDTLCSSLCSLEDGLLGSPARLASQLLGDE
LLLAKLPPSRESAFRSLGPLEAQDSLYNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER
QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTTCCCTGGCGCTCTGTTACACAAGCAAGATAAGCCAGCCCCACCTAATTTGTTCCCT
 GGCACCCCTCCTGCTCAGTGCAGACTGTACACTTAACCCATCTGTTCTCTAAATGCACGA
 CAGATTCCCTTCAGACAGGACAACACTGTGATATTTCAGGCTCTGATTGTAATACCTCTAAAG
 CCTGAAGCTTCTGTTACTAGCCATTGAGCTTCAGTTCTTCATCTGCAAATGGGCATAA
 TACAATCTATTCTTGCCACATCAAGGGATTGTTATTCTTAAACCAATACCAAAG
 AAGCTACAATGGCCTTAGCCAAAATTCTGTTGATTCAACGTTGTTTATTCACTTCT
 ATCGGGGAGGCATGGAAAAGAAAATCAAGACATAAACACACAGAACATTGCAAGAGTTT
 TTAAAACAATGGAAAATAACCTATTCTTGGAAAGTGAAGCAAACCTAAACTCAAGATAAA
 GAAAATATAACCACCTCAATCTCAAGGGAGTCATTCCCCTCTTGAATCTACCCAACAA
 CAGCCACGGAAATAACAGATTCTCAGTAACCTCATCAGCAGAGCATTCTGGGCAGTCTAA
 AACCCACATCTACCATTTCCAAGGCCCTTGTACATAGCTTGTAAAGTGCCT
 TGGAAATGCACCTATAGCAGATGAAGATCTTTGCCATCTCAGCACATCCAAATGTCACACC
 TGCTCTGCTTCAGAAAACITCACTTGGCTTTGTCATGACACCGTAAAAACTCTGTGATA
 ACAGTCCATTACAGTTAGCATCCTCTTCAGAACCAACTCTCCATCTGTGACCCCTTG
 ATAGTGGAAACCAAGTGGATGGCTTACACAAACAGTGTAGCTTCACTGGTTACCCCTTA
 TCAAGAAAAAAACACTCTACAGCCTACCTAAAATTCAACCAATAATTCAAAACTCTTCAA
 ATACGTCAAGATCCCAAAAGAAAATAGAAATACAGGAATAGTATTGCGGGCATTAGGT
 GCTATTCTGGGTGTCCTATGTTACTCTTGTGGCTACTGTGTGTTGAAAAGGAAAC
 GGATTCTTCCATGGCAGCTTATGACGACAGAAATGAACCAAGTGTGCGATTAGACA
 ATGCAACCGGAACCTTATGATGTGAGTTGGAAATTCTAGCTACTACAATCCAACCTTGAAT
 GATTCAAGGCAATGCCAGAAAGTGAAGAAAATGACGTGATGGCATTCTATGGATGACATACC
 TCCACTTCGTAATTCTGTATAGAACTAACAGCAAAAGGCGTTAACAGCAAGTGTCACTTA
 CATCCTAGCCTTGTGAAATTCTATCTTCAAAAGGTACACAAAATTACTGTCACTGGAT
 TTGTCAGGAGAATCATAAAAGCAGGAGACCACTAGCAGAAATGTAGACAGGATGTATCAT
 CCAAAGGTTTCTTCTTCAATTGGCCATCTGAGGCTTACTAAAGTAGCCTTAATT
 TGTATTAGTAGTATTCTTAGTAAAGGAAATTGGAAATTGAGGCAATGAAATGACAGACCTGTATT
 TCACCAATTACAGCCCTGCCTCATAACTAAATAATAAAAATTATTCACCAAAATTCTAA
 ACAATGAAGATGACTCTTACTGCTCTGCTGAAGCCCTAGTACCATATTCAAGATTGCA
 TTTCTTAAATGAAAATTGAAAGGGTGTGTTAAAGAAAATTGACTTAAAGCTAAAAGAG
 GACATAGCCAGAGTTCTGTTATTGGAAATTGAGGCAATGAAATGACAGACCTGTATT
 TAGTACGTTATAATTCTAGATCAGCACACACATGATCAGCCACTGAGTTATGAAGCTGA
 CAATGACTGCATTCAACGGGCCATGCCAGGAAAGCTGACCCCTACCCAGGAAAGTAATAGCT
 TCTTAAAGTCTCAAAGGTTTGGAAATTAACTGTCTTAATATATCTTAGGCTTCAA
 TTATTGGGTGCTTAAACATGAGAATCATGGT

FIGURE 24

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISELESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFPNTSDPQKENRNTGIVFGAILGAIL
GVSLLTIVGYLLCGKRKTDTSFSHRRLYDDRNEPVRLDNAPEPYDVSGFNSSYYNPTLNDSA
MPEESEENARDGIPMDDIPLRTSV
```

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCCTTGCA GTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
 AGCCCCGAAGATTCACT**ATGGT**GAAAATCGCCTTCATAACCCCTACGCCGTGCAAAGGAGG
 AGGCGCGGCAAGACGTGGAGGCCCTCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAGAGGGCTCTGGGAGATGTATGCTTACTCT
 CTTAGGCCTTCATTCATCTGGCAGGACTATTGTTGGTGGAGCCTGCATTTACAAGTACT
 TCATGCCAAGACGACCATTACCGTGGAGAGATGTGCTTTTGATTCTGAGGATCCTGCA
 AATTCCCTCGTGGAGGAGGCCAACCTCCTGACTGAGGAGGCTGACATTGCGA
 GGATGACAACATTGCAATCATTGATGTGCCGTCCCCAGTTCTGATAGTGACCCCTGCA
 CAATTATTATCATGACTTTGAAAAGGAAATGACTGCTTACCTGGACTTGTGCTGGGAACTGC
 TATCTGATGCCCTCAATCTATTGTTATGCCTCAAAAAATCTGGTAGAGCTTTGG
 CAAACTGGCGAGTGGCAGATACTGCCTCAAACATTATGTTGCTGAGAAAGACCTAGTGCTG
 TGGAGGAAATTCTGTGATGTTAGTAACCTGGCATCTTATTACCAACTTGCAATAACAGA
 AAAGCTTCCGCCTCGTCGCAGAGACCTCTGCTGGTTCAACAAACGTGCCATTGATAA
 ATGCTGGAAGATTAGACACTTCCCAACGAATTATTGTTGAGACCAAGATCTGCAAGAGT
AAAAGGCAACAGATAAGTGTCTTGGATAAAGAAGTCAGAGATTACAATATGACTTAA
 CATTAAAGGTTTATGGGATACTCAAGATAATTACTCATGCATTACTTATTGCTTATGCTT
 AAAAAAAGGAAAAAAAAAAACTACTAACCAACTGCAAGCTTGTCAAATTAGTTAAT
 TGGCATTGCTTGTGTTTTGAAACTGAAATTACATGAGTTCATTTCTTGCATTATAG
 GGTTAGATTCTGAAAGCAGCATGAATATACACCTAACATCCTGACAATAAATTCCATCC
 GTTGTGTTTTGTTGTTGTTCTTTCTTAAAGTAAGCTTTATTCTATGCTTATG
 GTGGAGCAATTAAATTGAAATATTAAATGTTGAACTTTGTGAAATTATA
 TCAGATCTCAACATTGTTGTTCTTTGTTTCATTGTACAACCTTCTGAAATTAGA
 AATTACATCTTGCAGTTCTGTTAGGTGCTGTAAATTAACTGACTTATATGTGAAACAATT
 TTCATGAGACAGTCATTAACTAATGCAGTGATTCTTCTCACTACTATCTGTTG
 AATGCACAAAATTGTGTTAGGTGCTGAATGCTGTAAGGAGTTAGGTGATGAAATTCTACAA
 CCCTATAATAATTACTATACAAAAA

FIGURE 26

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
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MVKIAFNTPTAVQKEEARQDVEALLSRTVRTQILTGKELRVATQEKEGSSGRCMLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVVPVPSFSDPAAIIHDFEKGMTAYLDLLLGNCYLMLPLNTSIVMPPKNLVELFGKLASG
RYLPQTYYVVERDLVAVEEIRDVSNLGIFYQLCNNRKSFRLLRRDLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE
```

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGAGGGAGGGAGGGCGGGCAGGCGCCAGCCCAGAGCACGCCCCGGGCACCAGCACGGACTCTCT
 CTTCCAGCCCAGGTGCCCCCACTCTCGCTCATTGGCGGGAGCACCCAGTCCTGTACGCC
 AAGGAACCTGGTCTGGGGCACC**ATGGTT**CGCGCAGCCCCAGCCTCTCATCCTCTG
 TTGCTGCTGCTGGGTCTGTGCGCTGCTACCGACGCCGCTCTGTGCCCTGAAGGCCACGTT
 CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCAGGGCTGTCGCCCTCCCGAGGCC
 CGCCACCTGGACCCGGCCCTCAGCCCCACATCGATGGGCCAGCCCACAACCTGGGG
 GGCCCACATACCCCCACCAACTCCTGGATGGGATAGTGAACTCTCCGCCAGTACGTGAT
 GCTGATTGCTGTGGTGGCTCCCTGGCCTTCTGCTGATGTTATCGTCTGTGCCCGGTCA
 TCACCCGGCAGAAGCAGAACAGGCTCGCCATTACCATGTCCTCCCCAAGAAGAAGTAC
 GTGGACCAGAGTACCGGGCGGGGGCCCCGGGCTTCAGTGAGGTCCCCGACAGAGCCCC
 CGACAGCAGGCCAGGAAGCCCTGGATCCTCCGGCAGCTCAGGCCACATCTTGGCG
 CCACCCAGAACCTCAAGTCCCCACCAGGGCTGCACTGGCGGTGGGACGGAGCCAGGATG
 GTGGAGGCAGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGACAGGAAGTCCA
 GGGACATGGGTCCCAGTGGAGACACCAGGGCGCAGGAGGAGCCGTGTCAGGGTCTTG
 AGGGGCTGTGGTGGCCGGTAGGGCCAAGGGGAGCTGAAAGGGTCTCTTGTAGCCCAG
 GAAGCCCAGGGACCAGTGGTCCCCCGAAAGCCCCGTGCTGCAGCAGTGTCCACCCCCAG
 TGTC**TAA**CAGTCCTCCGGCTGCCAGCCCTGACTGTCGGGCCCAAGTGGTACCTCCCC
 GTGATGAAAAGGCCCTCAGCCCTGACTGCTTCCTGACACTCCTCCTGGCTCCCTGTGG
 TGCAATCCACGATGTGCTGATTCTACAGCAGGCAAATGCTGGTCCCCTGGCCCTGG
 GGAATCTACCAAGTGCCATCATCCTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC
 ACAGCTCCCTGACAAAGTGAGGGAGGCCACGTGTCCTGTGACAGCCAGATAAAACATCC
 CCCAAAGTGTGGATTACAGGCGTGAGCCACCGTGCCCCGCCAAACTACTTTTAAACACA
 GCTACAGGGTAAATCCTGCAGCACCCACTCTGAAAATACTGCTCTAATTTCCTGAAGG
 TGGCCCCCTGTTCTAGTTGGTCCAGGATTAGGGATGTGGGTATAGGGCATTTAAACCTCC
 TCAACCGCTCTCAAGCACCCCGGCCCTGGGGTGAGTTCTCATCCGCTACTGCTGCTGG
 GATCAGGTTGAATGAATGAACTCTTCCTGTCTGCCCTCCAAAGCAGCCTAGAAGCTGAGGG
 GCTGTGTTGAGGGACCTCCACCCCTGGGAAGTCCGAGGGGCTGGGAAGGGTTCTGACG
 CCCAGCCTGGAGCAGGGGGCCCTGGCACCCCTGTGCTCACACATTGTCGGCAGCCTG
 TGTCCACAATATTGTCAGTCCTCGACAGGGAGCCTGGCTCGCTGCTTAAAGGGAGGCT
 CTGGCAGGGAGGTCTCTCCCCCATCCCTCATCTGGGCTCCCCAACCTCTGCACAGCTCT
 CCAGGTGCTGAGATATAATGCACCAGCACAATAAACCTTATTCCGGCCTGAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 28

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLLLLLLLGSVPATDARSVPLKATFLEDVAGSGEAEGSSASSPSLPPPWTPAL
SPTSMGPQPTTLGGPSPTNFLDGIVDFFRQYVMLIAVVGSIAFLMFIVCAAVITRQKQKA
SAYYPSSFPKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEKGSQEGDQEVTQGHGPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLQAQEAQGPVGPPESPCACSSVHPSV
```

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

FIGURE 29

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA
 GGGAGGACAGGGAGTCGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG
 GCAAGGAGGAGACCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGCTGGCAGAG**ATG**
 AAGTTCCAGGGGCCCTGGCCTGCCTCTGCTGGCCCTCTGCCTGGCAGTGGGAGGCTGG
 CCCCTGCAAGCGAGAGGAAGAACACTGGACAAATTATGGGAGGCCCTGGACATGCC
 TGGGAGCCCCCTGAGCGAAGGGTGGAAAGGCCATTGCAAAGAGGCCAGGGCAGCT
 GGCTCTAAAGTCAGTGAGGCCCTGGCCAAGGGACAGAGAAGCAGTTGCACTGGAGTCAG
 GCAGGTTCAGGCTTGGCGCAGCAGATGCTTGGCAACAGGGTGGGAAGCAGCCATG
 CTCTGGAAACACTGGGCACGAGATTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCA
 GATGCTGTCGCGGCTCTGGCAGGGGGCTGGCACAGTGGCTTGGAAACTCTGG
 AGGCCATGGCATTTGGCTCTCAAGGGCCTTGGAGGCCAGGGCAATCTGGAG
 GTCTGGGACTCGTGGGTCACGGATAACCCCGAAACTCAGCAGCAGCTTGGAAATGAAT
 CCTCAGGGAGCTCCCTGGGTCAAGGAGGAATGGAGGGCCACCAAACCTTGGACCAACAC
 TCAGGGAGCTGTGGCCCAGCCTGGCTATGGTCAGTGAGAGGCCAGCAACCAAGAATGAAGGGT
 GCACGAATCCCCCACCATGGCTCAGGGAGGCTCCAGCAACTCTGGGGAGGCAGCGGC
 TCACAGTCGGGAGCAGTGGCAGTGGCAGCAATGGACAACAAACATGGCAGCAGCAGTGG
 TGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGGGCAGCAGTGGGGCAGCAGTGG
 GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGTCCTCTGGGA
 TCCAGCACCGGCTCTCCGGCAACCACGGTGGAGCGGGAGGAAATGGACATAAAC
 CGGGTGTAAAAGCCAGGAATGAAGCCCGGGAGGGGAATCTGGGATTCAAGGGCTCA
 GAGGACAGGGAGTTCCAGCAACATGAGGGAAATAAGCAAAGAGGCCAATCGCCTCTTGA
 GGCTCTGGAGACAATTATCGGGGCAAGGGTCAGCTGGGCAGTGGAGGAGGTGACGCTGT
 TGGTGGAGTCAAACTGTGAACCTGAGACGTCTGGGATGTTAACCTTGACACTTCT
 GGAAGAATTAAATCCAAGCTGGGTTCATCAACTGGGATGCCATAAACAGGACCAAGAGA
 AGCTCTGCATCCCG**TGAC**CTCCAGACAAGGAGGCCAGATTGGATGGAGCCCCACACT
 CCCTCCTTAAACACCACCCCTCTCATCAACTATCTGCCCTTGGGATGCCATAAACCTTA
 GCTGCCCAAA
 AAA

FIGURE 30

```
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><subunit 1 of 1, 440 aa, 1 stop
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MKFQGPLACLLLALCLGSCEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVQRQVPGFGAADALGNRVEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGLGGQQGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPSGSGGGSSNSGGGS
GSQSGSSGSGSNGDNNNGSSGGSSGGSSGGSSGGSSGGSSGNSGGSRGDSGSESSW
GSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLL
GGSGDNRYRGQGSSWGSGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ
```

RSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 31

FIGURE 32

MCFLNKLLLLAVLGWLQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC
CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTSLGAQPSQTSQQLQAQAFFHNQPP
SLRRTVEFVAERIGSNCVKHIKATLVALVRQAESLLQEQLVTQGEEGGDPAAQLLEILCSQL
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL
IRREVKAASRTLRAQGPEPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGTCTGGTGGCTGGTCGGGCTACTGAAGGCTGTTGATCAGGAAACTG
 AAGACTCTCTGCTTTGCCACAGCAGTCTCTGCAGCTCTTGAGGTGTGAACCCACATCCC
 TGCCCCCAGGGCACCTGAGGACGCCAACCTACCCCTCAGCAGACCCGGAGAGAA**ATG**
 ACTAGCAACAAGAGCAGCGTCAGCAGTGTCTGTATCCTCTTGCCCTCATACCATCCT
 CATCCTCTAAGCTCAAACAGTGCCTAAGAGTGGAGCATCCTGACGGCTATGTCCCCATTCTCGGC
 GCCGGCGGACCTGTCAACCTCAAGAAGTGGAGCATCCTGACGGCTATGTCCCCATTCTCGGC
 AACAAAGACACTGCCCTCTGGTGCCACAGTGTGTAGTGTAGCAGCTCCAGCACCTGCT
 GGGCACCAAGCTGGGCCCTGAGATCGAGCGGCTGAGTGTACAATCCGATGAATGATGCAC
 CCACCACTGGCTACTCAGCTGATCTGGGCAACAAGACCACTACCGCGTGTGGCCCATTC
 AGTGTGTTCCCGCTGCTGAGGAGGCCCCCAGGAGTTTGTCACCGGACCCCTGAACCGTGT
 CATCTTCTGGGGGCCCGAGCAAGATGCGAAGACCCCAAGGGCAGCCTGTGCGTGTGATCC
 AGCGAGCGGGCCTGGTGTCCCCAACATGGAAGCATATGCCGTCTCTCCGGCCGATGCGG
 CAATTTGACGACCTCTCCGGGGTGGAGACGGGAAAGCAGGGAGAAGTCTCATCTGTGTT
 GAGCACAGGTGTTTACATGGTATCGCGGTGAGTTGTGTGACCACGTGATCTATG
 GCATGGTCCCCCAACTACTGCAGCAGCGGCCCGCCCTCAGCGATGCCCTACCAACTAC
 TACCGAGGCCAAGGGGCCGAGCAATGTGTCACTACATCCAGAAATGAGCACAGTCCAAGGG
 CAACCAACCCACCGCTCATCACCAGAAAAGGGTCTTCATCGTGGGCCAGCTGTATGGCA
 TCACCTTCTCCACCCCTCTGGGACT**TAGGCCACCCAGCCCTGGGACCTCAGGAGGTCAG**
 AGGAGAAGCAGCCTCCGCCAGCCGTAGGCCAGGGACCATCTCTGGCCAATCAAGGCTTG
 CTGGAGTGTCTCCAGGCAATCAGGGCTTGGAGGAGATGTATCTCCAGCCAATCAGGCC
 GGCTTGGAGATCTTGGGCAATCAGGGATTGGGGATCTATGTGTTAATCAGGGGTGTCTTTC
 TTGTCAGTCAGGGTCTGGCACAGTCATCAGGGTAGAGGGGGTATTCTGAGTCATCTG
 AGGCTAAGGACATGTCTTCCCATGAGGCCCTGGTCTAGAGCCCCAGGAATGGACCCCCA
 ATCACTCCCCACTCTGTGGGAAATGGGTCTGTCCAAGGGAGCTGGGAAACTTGGGTGTTG
 CCCCTCAATTCCAGCACCGAAAAGAGATTGTGGGGCTAGAAGCTGTCTGGGCC
 GGCCAGAGAATTGTGGGGTGTGGAGGTGTGGGGCGGTGGGGAGGTCCCAGAGGTGGGA
 GGCTGGCATCCAGGGTCTGGCTCTGGCTGAGACCTTGGACAAAACCCCTCCCCCTCTGGG
 CACCCCTCTGCCACACCAAGTTCCAGTGGCAGGTCTGAGACCCCTTCCACCTCCCCACAA
 GTGCCCTCGGGTCTGTCTCCCGTCTGGACCCCTCCAGGCCACTATCCCTGCTGAGGCT
 CAGCTTTGGGGGCTGGGTGACCTCCCCACCTCTGGAAAAACTTGGGTATTGTC
 GCAAACCTCTCAGGGTTGGGGACTCTGAAGGAAACGGACAAAACCTTAAGCTGTTTCT
 TAGCCCCCTCAGCCAGCTGCCATTAGCTGGCTCTAAAGGCCAGGCCCTCTTTCTGCCCT
 CTAGCAGGGAGGTTTCAACTGTGGAGGCGCTTGGGCTGCCCTTGTCTGGAGTC
 CTGGGGGCTCCGAGGGTCTCCCTGACCCCTCTGTGCTCTGGGATGGCTGTCGGAGCTGT
 ATCACCTGGGTCTGCCCCGGCTGTATCAGGCACTTATAAAGCTGGCCCTAGTGG
 GGTGTGTTGTCTCTGCTCTGGAGGCTGGAGGAAAGGGCTCAGGAGGAGGCTGTGA
 GGCTGGAGGGACCAGATGGAGGAGGCCAGCAGCTAGCATTGCACACTGGGTGATGGGTGG
 GGGCGGTGACTGCCCTGGGTTGTAAATGATTGTACAGGAATAAACACACCTACGC
 TCCGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 34

MSSNKEQRSAVFVILFALITILYLSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL
GNKTLPSRCHQCIVSSSSHLLGTKLGPPIERAECTIRMNADPTTGYSAADVGNKTTYRVVAH
SSVFRVLRRPQEJVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFPNMEAYAVSPGRM
RQFDDLFRLFRGETGKDREKSHSWLSTGWFTMVIATELCDHVHVYGMVPPNYCSQRPRLQRMPYH
YYEPKGDPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

FIGURE 35

FIGURE 36

MLRGTMATAWRGMRPEVTLACLLLATAGCFADLNVEPVQVTVPASTVQKPGGTIVLGCVVEPP
 RMNVTVRLNLNGKEELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHPKAQVRYSVKQEWLEASRGNYLIMPSGNLQ
 IVNASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRSTAEEAARIIYPPEAQTIIVTKGOSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTSEEDSGTYRCMADNGVGQPGA
 AVILYNVQVFEPPEVTMELSQLVIPWGQSAKLTCERVGNPPPSVLWLRNAVPLISSQLRLS
 RRALRVLSMGPEDEGVYQCMAEENEVGSAAHVQQLRTSRPSITPRILWQDAELATGTPVSPSK
 LGNPEQMLRGQPALPRPPTSVGPASPCKCPEKGQGAPAEAPIIILSSRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFRTGRRPKPEIMASKEQQIQRRDDPGASPQSSSQPDHGRLSPPEAPDRPTISTASE
 TSVYVTWIPRGNGGGFPIQSFRVEYKKLKVGDWILATSAPIPPSRLSVEITGLEKGT SYKFRV
 RALNMLGESEPSAPSRRPYVSGYSGRVYERPVAGPYITFTDAVNELLMLKWMYI PASNNNT
 PIHGFYIYYRPTSDNDNSDYKKDMVEGDKYWHISHLQPETSYDIKMQCFNEGGESEFSNVM
 ICETKARKSSGQPGRLPPP TLAPPQPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVL
 IIIVTFIPFCLWRAWSKQKH TDLGFPRLS ALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRCGPSAAGVYPMKPQHQHCPGELOQQSDTSSLLRQTHLGNGYDPQSHQITRGPK
 SSPDEGSFLYTLPPDDSTHQLLQPHHDCCQRQEOPAAGQSGVRRAPDSPVLEAVWDPPFHSG
 PPCCLGLVPVEEVDS PDSCQVSGGDWC P QHPVGAYVCQEPGMQLSPGPLVRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGTCGTATGATCCGGACCCATTGTCGGCCTCTGCCCATGCCCTGCTCCTC
 CCAGGCTCCCGGGCGACCCCCGCGCAAC**TG**CAGCCCACGGGCCGAGGGTCCCGC
 GCTCAGCCGGCGGTATCGGGCGTCTGCTGCTCTGCTACTGCTGCTGCTGCCGAGC
 CCGTAACCCCGCGGAGACCAACGCCGGCGCCCCAGAGCCCTCTCCACGCTGGCTCCCC
 AGCCTCTTCAACCACGCCGGGTGTCCTCACGCCCTCACTACCCCAGGCCTCACTACGCCAGG
 CACCCCCAAAACCCCTGGACCTCGGGTGCAGGCCGAGGCCCTGATGGGAGTTCCCACTCG
 TGGACGGCCACAATGACCTGCCCCAGGTTCTGAGACAGCCTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTCAGCCATGGTCAGACCAGCCTGGACAGGTTAGAGACGCCCTCGT
 GGGTGCCAGTTCTGGTCAGCCTCCGTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC
 TCGCCCTGGACAGATTGACCTCATTACCGCATGTGTGCCCTACTCTGAACTCGAGCTT
 GTGACCTCAGCTGAAGGCTGAACAGCTCTAAAGCTGGCCTGCCCTATTGGCGTGNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTGTGCTGCCAGTTCTATGTGCTGGGGTGCCTG
 ACCTGACACTTACCTTCACCTGCAGTACACCATGGGAGAGAGTTCCACCAAGTTCAGACAC
 CACATGTACACCAACGTCAGCGGATTGACAAGCTTGGTGAGAAAGTAGTAGAGGGAGTTGAA
 CCGCCTGGGATGATGATAGATTGCTTATGCATGGACACCTTGATAAGAAGGGTCCCTGG
 AAGTGTCTCAGGCTCTGTGATCTCTCCACTCAGCTGCCAGAGCTGTGTGACAATTGG
 TTGAATGTTCCCGATGATACCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT
 GTCCATGGGGTGCAGTCAGTGCACCTGCTGCTAAGCTGCACTGTGGCAGATCACTTTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGATTGGTGGAAATTATGACGGGACT
 GGCGGTTCCCTCAGGGCTGGAGGATGTGTCCACATACCCAGCTGTGATAGAGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCTTCTGTGAAACCTGCTGCCGTCT
 TCAGACAAGTGGAAAAGGTGAGAGAGGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTT
 CCATATGGGCAACTGAGCACATCCTGCCACTCCACCTCGTGCCTCAGAATGGACACCAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCTGGAGGTCCCAAATGCC
 CCCCATACCTGTTCCAGGCCTTGTGGCTGCTGCCACCATCCCAAACCTTCACCCAGTGGCTC
 TGCT**G**AACAGTCGGTCCCCCAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCC
 AGTTCAATTACAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

FIGURE 38

```
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><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
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ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRFSHQ
TSLDRLRDGLVGAQFWASAVSCSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSDLSSLVLSFYVLGVRYLTLCFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSSYASDTLIRRVLLEVSQAPVIFSHSAARAVCDNLLNVPPDILQL
LKNGGIVMVTLSMGVLQCNCNNANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIIEELLSRXWSEEELQGVLRGNLLRVFRQVEKREESRAQSPVEAEFPYGQLSTSCH
SHLVPQNQHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
 TCCCTATGACTGCAATGTGAGGTGTCGGGCTTGCCTGGCCAGCAAGCCTGATAAGC**ATG**
 AAGCTTTATCTTGGCTGTGGCTGGGTTGCTGGTGCCTGGCCAGCTGAAGCCAACAA
 GAGTTCTGAAGATATCCGGTGAAATGCACTGTCCACCTTATAGAAACATCAGTGGCACCA
 TTTACAACCGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGGTGGAGCCATGCCA
 GTGCCTGGCCATGACGTGGAGGCCACTGCCTGCTGCGAGTGCAGGTACGAGGGAGCGAG
 CACCACCAACATCAAGGTATCATTGTATCTACCTGTCGCTGGTGGGGTGCCTGTTGCTCT
 ACATGGCCTTCTGATGCTGGTGGACCCCTGATCCGAAAGCCGGATGCATAACTGAGCAA
 CTGCACAATGAGGAGGAGAAATGAGGATGCTGCTCTATGGCAGCAGCTGCTGCATCCCTGG
 GGGACCCGAGCAAACAGTCTGGAGCGTGTGAAGGTGCCAGCAGCGGTGGAGCTG
 AGGTGCAGGAGCAGCGGAAGACAGTCTCGATCGGCACAAGATGCTCAGC**TAG**ATGGCTGG
 TGTGGTTGGGCAAGCCCCAACACCATGGCTGCCAGCTCCAGGCTGGACAAAGCAGGGGG
 CTACTTCTCCCTCCCTCGTTCCAGTCTCCCTTAAAGCCTGTGGCATTTCCTCCTT
 CTCCCTAACTTTAGAAATGTTGACTTGCTATTGATTAGGAAAGAGGGATGTGGTCTCT
 GATCTCTGTTGCTCTTGGTCTTGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA
 ATGGAGACATTCGAGGCCCTCAGGAGTGGATGCGATCTGCTCTGGCTCCACTTTG
 CGCCTCCAGCTCTGAGTCTGGGAATGTTGTTACCCCTGGAAAGATAAGCTGGTCTCA
 GGAACTCAGTGTCTGGAGGAAAGCATGCCAGCATTAGCATGTTCTTCTGCAGTG
 GTTCTTATCACCACCTCCCTCCAGCCCCGGCGCTCAGCCCCAGCCCCAGCTCCAGCCCTG
 AGGACAGCTCTGATGGGAGAGCTGGCCCTGAGCCACTGGTCTCAGGGTGCAGTGG
 AGCTGGTGTTCGCTGTCCCCCTGCACTTCGCACTGGGCATGGAGTGCCCATGCATACT
 CTGCTGCCGGTCCCTCACCTGCACTTGAGGGGTCTGGCAGTCCCTCTCCCCAGTGT
 CACAGTCACTGAGCCAGACGGTGGTTGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
 CACCCAGCCCCCTGACTTGGGTTGCCCTTGTCCCTGAAACTCGTTGACCGTGCATGGA
 GAGAAAATTTGTCTCTTGCTTAGAGTTGTGTAAATCAAGGAAGCCATCATTAAATTG
 TTTTATTCTCTCA

FIGURE 40

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
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<MW: 20574, pI: 6.60, NX(S/T): 3
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PVPGHDVEAYCLLCECRYEERSTTIKVIIVIYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAASLGGRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

AGGGGGTCTCGCTGGGTCGGCTAATCTGTCTGAGGGTGTAGAGTCAAGGGTCTGGGGTCCCCGA
 ACCAGGAAGGGTGAGGGAACACAACTCTGCAAGCCCCCGCAGCCAAAGTGAGGGGCCCGTGTGGGTCTCTCCC
 TCCCTTGCATTCACCCACCCCTCGGGCTTGTGCTTCTGGGACCCCTCGCGGGAGATGGCCCGGTGATG
 CGGAGCAAGGATTCGCTCTGCTGGCTCCACTGAGGGCTGCTGATGGTGGAGAGCTCACAGATCGCAGT
 TCGCGGGGCCAACATCAACTCATCAAGTCTCTGGCGGGAGAGCGCTGGTCAGGCCCAATCGATCTCG
 GGCGATGTAACAAAGGACTGGCATTCGGCGGCACTGAAGAAGGCAAACCTGGGGCAAGGCCAACCTTGACCGAT
 GATAAAGGAGTGTGAGGTGGAGGAGTATTGCGCAAGTCCGGCTGGCATGTCAGCCCTGCAATAATGGCATCTGATCCAGTT
 AAAAGAAGGCGCTGCCACCGAGATGGCATGTCAGCCCTGCAATAATGGCATCTGATCCAGTT
 ACTGAAAGCATCTAACCCCCCTCACATCGGGCTGGTACTCGGCAGAGATCGAACACAGCTGATTAC
 TCAAAACCATGACTTGGGATGGCAAGATCTGAAGAACACACAATGATGCAACATATAAAAGGCGATGAGGA
 GACCCCTGCCACTGAGATCATCGACTGCAATTGGGTTTGTGCTGCTGCTCATTTCTGGACCAAAATCTGCAAA
 CCAGTGTCCATCAGGGCTGCTGCAACACAGCAAGGGGTTCTATGGCTGAAATTTCCAGCGT
 TGGCAGCTGTGGAGGGCTGCTGCAAGATATGGGAAAGATGCCACTACTCCTCCAAAGCCAGACTCATGTG
 TGTGAGAAAATTGATGACCTGGAGGACATCTGCAATTGAGCTGGTACTCGGAGTGTGATTTAATGCTTATAG
 CATGGTGGAAAATTAAGGTCAGATCAGAGAATGGCTAAAAAAGAAGACGTGATAAAATAGATGATCACAA
 AAAGGGAAAAGAACATGACATGAACTGAGTAAAGTGGGTGACAAATGAGCTGGCAGTGCAGCAGTCTTCCATTATG
 CAACITGCTCATGTAATAATGCAACATTGGGAAATGCTTATTAAGGAAACAGCACAGTGGAAAAT
 ACTGATGAGTACATGTGACTTCAAGGTTAGGTTGCTGGAGGAGGGTTCTCAGATTGCTGATTG
 TTATACAAATACATGCACTGGCAGATTCTATTCACCTGAGTAAAGGAAATACTCTGAGTCTTAA
 CAACTAGGTTCAAAAATTAAGGCTGCTTCAACAGTGGCTTCAATGAGCTGGTGTGAGTAAAGGAAAT
 TACCTTTTGATTGTAAACTACTTCTGCTGTCATCAAGGCTGGTGTGAGTAAAGGAAATTCAGTCAAT
 TTCCAATAATGGCAAAATATGGCCAGTGTGTTAGGAAGGCCCTTAGGAAGGACAAAATAAACAAACAG
 CCACAAAATCTTTTCAAAAATTGTTACCTGTAATTAAAGAACTGATACAAGAACAAAAGCTTC
 TCTCAGGTTCTGGAAATGACAGTATCTCTCTTCACTGATGTTCAAGGTTTCTGAGTGGCTTCA
 AACTACATCACTTAATTGACTGAAATTAACAGGTTTCTGAGGATGCAAGGTTTCAAGGTTTCTGAGTGGCTTCA
 GATGTCAGGAAATGTCAGGAAAGACCTGAGGAGATCATTGTTCTTAAAGGTTGGCCATAACCTTATTT
 TAGATAAATTGTTGAAATACATCTATCATACACTCTGTTGTCAGGTTTGGCAACACATAGATCATATGCTG
 CACTGAGGTAAGCAAAATTGGGAAACTTTCGTTGTCAGGTTTGGCAACACATAGATCATATGCTG
 AGGCACAAGTTGGCTGTTCACTTGAACACAGCTAAATGAAATCTGCACTGGGATTGAGCTTAA
 CATATAATTACTACTGCAAGTGAATTGACTGAGGTTCTGTCAGTACTATCTCAAAATTATTTATAG
 TGCTGAGATCTCAAAATCTCAATTTCAGGAGGTTTCAAAAATGACTCTGAGTACAGAGTAGTGTGAGG
 TTTCAATTGCCCTCTATAAGCTCTGACTGCAATGCGCATCATCCTTTCTCCCAAACCTCTGCAACATCTG
 CTTTATTGCAAAGGCTAGTTGCGTTCTGCAAGCATTGGGTTAAAATTAAGTGAAGTAACTTGTAAA
 ACCTGCAATTGCTTAATCTAGACACACAGTTCTAAATTCTTTGAAACACTTACTTAACTTTAAACT
 AACTCAGTTCTAAATACTTTGCTGGAGCAACAAAATAAAAGGTTTCTATAGTGTGACTTAAACTTTG
 TAGACCAAAATTGACTTTTACTTAATGCTTCAACAGGTTCTGAGTCTCAAAATTAAAGTCTCCAGTAG
 AGATTGAGTTGAGGCTGATATCTATAAAATTCTCAACTTCCACATATATTACTAAAGTGAATTAAGCTTA
 CATTTCGCAAGGCTGCAAAAACAAAATTATAAAACTGTCATCAGGAAACCAAGTTGTATAAACAGGT
 TGCTATAAGGCTGTGAAATGAAAATGGAACATTCAATCAACATTCTCTATATAACAAATTATTATTTACAAAT
 TTGGTTCTGCAATATTCTATGTCACCCCTTAAAATTAATTATTGAGTAATTATTACAGGAAATG
 TTGTAATTAGGAAAATGATATAAGATAAAATTCTACAGAAGCTTGTAGCAGAATATAATTGAGCTTATTGAC
 AAAA

FIGURE 42

MAALMRSKDSSCCLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQGSSACMVCRKKRCHRDGMCCPSTRCNN
GICIPVTEISILTPHIPALDGTRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCRLS
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
SKARLHVCQKI

Signal peptide:

amino acids 1-25

1 ab
2 ab
3 ab
4 ab
5 ab
6 ab
7 ab
8 ab
9 ab
10 ab
11 ab
12 ab
13 ab
14 ab
15 ab
16 ab
17 ab
18 ab
19 ab
20 ab
21 ab
22 ab
23 ab
24 ab
25 ab

FIGURE 43

TCTCAATCTGCTGACCTCGTATCCGCCTGACCTTGTAAATCCACCTACCTGGCCTCCAAA
 GTGTTGGGATTACAGGCCTGAGCCACCAGCAGCCAAACATCACGTTTAAAAATTGATT
 TCTTCATAATTCATGGCAAATATTCCTTCCCTTAACTCTTATGTCAGAATGAGGAAGGA
 TAGCTGCATTATTTAGTCAGTTTCAATTGCACTAGAATATTTCATGAGTATTCTAAG
 TTATATTTAGTAATTCAATGTTTAGATTAGTGTAAACATACTTGAAAGAAATACTTG
ATGTGTAAAGCTTAAAGCTTGGGAGAAATCTGTATTGTTGAGATTGTTCTTATCCCCCT
 TTTAAAGTCATCCGTCTGGCTCAGGATTGGAGAGCTGCACCACAAAAATGCCAAC
 TCACCAAGCTCCAGATTGGACCAGTGAAGCTCCAGTTGGCAGTTTACCAACCACC
 CCAAGTACACAGCAGAAATAGTACAAGTCACCTACAACTACTACTCTGGACCTCAAGCC
 CCCAACATCCCAGTCCTCAGTCATCTGACTCAAATCTCAACCTGAGCCATCCC
 CAGTTCTAGGCAGTGAGGCCAGCAGCACACAGCACCAGAGCCAGGCAGTCACTGTTCTCCT
 CCTGGTTGGAGTCCTTCTTCCAGGCAAAACTTCAGAATCAACACCTGGAGACAGTC
 CTCCACTGTGAACAAGCTTTGAGCTTCCAGCAGCAGCATTGAAAATATCTGTGCTG
 TCCACCAGCCACAGCCAAACATCAAATGCTAAGCGCGGATACCCCCAGCTCTAA
 ATCCCCAGCTCTGCAGTGGAAATGGCTGAGCTTCTCTGAGATTGGATCAGCTCCAAGCAGT
 TGGGGCTCTGGAATTGGGTAGAACCTCTCTCTGAAATTGGATCAGCTCCAAGCAGT
 AAAATAGTAATCAGATCCCCATCAGCTTGATTGAAAGCTTAAAGTGGACCTTGAAATACA
 TCTTTATCAATGACCACTGCACTGAGTCAGAATCCACATATAACACTCCGTCAATTACCTCCTG
 CAGTCTGACAAGCTCATCAGTGAATTCTGCTAGTCCAGTAGCAATGCTTCTCTTATGACC
 AGAGTTCTGTGCATAACAGGATCCCATACCAAAAGCCCTGTGAGTTCATCAGACTCAGCTCCA
 GGAACCATCATGAATGGACATGGCTGGTGGCGAAGTCAGCAGACACTAGACAGTAAGTATAG
 CAGCAAGCTACTTGTCTGGCTGGTGGCGAAGCAACCAACAGAGGAAGAGGATAGCTACGTGA
 TGTGGAAAACACCAGTGGCTGTCATGGCTATTGCTCATGGCTATTGCT
TAAAAGCAGCCCTTGTCTTGT
 TTTGGACCAAGGTGTTGGCTGTGGTGTATTAGAAATGCTTAACACAGCAAGAAGGAGGT
 GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCCACAAGTGCACTACAGTATGCAT
 TTTAAAGATGCTTGGCCAGGCGGGGTGGCTGATGCCATAATCCCAAGTGCCTTGGGGGCC
 AAGGCAGGCAAGATTGCCAAGCTCAGGAGTTGAGACCAACCTGGCAACATGGTAAACTC
 TGTCTCTACTAAAATACGAAAAACTAGCCGGGTGTGGTGGCGCGCTGCTGAAATCCAG
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTGGCTACAAAGTGAAGACTCC
 GTCTGAAAAGA

FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPP
PGLESFPSQAKLRESTPGDSPSTVNKLQLPSTTIENISVSVHQPKHIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTSVITCSLTSSSLNSASPVAMSSSYDQSSVHNRIPYQSPVSSSESAP
GTIMNGHGGGRSQQTLDSKYSSKLLSWLVPTKQRKRIAHVMWKTPVGQWLIR

Signal peptide:

amino acids 1-24

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24

FIGURE 45

GCCGAGTGGGACAAAGCCTGGGCTGGGGGGGGCC**ATG**GCGCTGCCATCCGAATCCTGCT
 TTGGAAACTTGTCTTCGAGAGCTCTGCTGTTCTCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCCGCTGGAGGTACCGACGGCCCCCGGCCACCCCCGCTACTGGGACGGCAGAAGGA
 GGTGCTGGCGGTGGCGCGCGCACCCGCTCTGACCTGCGTGAACCGCGGGCACGTG
 GGACCGACCGGCACGTGGAGGAGGCTAACAGGTGGTCACTGGGACGGCAGCCGGGG
 GTCCCGACGACCGCGCGGACCCGCTGCTGGACCTCTACCGCTGGCGAGGCCGCCCTA
 CGGGCCCTTTTCTGCGCGACCGCGTGGCTGTGGCGGGATGCCTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCAGCAGGGCACCTACTCCTGCCACCTGCAC
 CACCAATTACTGTGGCCTGCAACGAACGCCGCTTCCACCTGACGGTCGCCAACCCCACG
 GGAGCCGCCCGGGGCTCTCCGGCAACGGCTCAGGCCACAGCGGCCAGGCCAGGCCAG
 ACCCCCACACTGGCGCGGGCACAACGTCAATGTATCGTCCCCAGAGGCCAGGCCAC
 TTCTTCAGCAGCTGGCTACGTGCTGGCACGCTGCTCTTCATCCTGCTACTGGTCAC
 TGTCTCCTGGCCGCCGCAGCGCCGGAGGCTACGAATACTCGGACCAGAAAGTCGGAA
 AGTCAAAGGGGAAGGATGTTAACCTGGGGAGTCGCTGTGGCTGCAGGGGACCAGATGCTT
 TACAGGAGTGAGGACATCCAGTAGATTACAAAAACACATCCTGAAGGGAGAGGGCGGAGCT
 GCCCCACAGCCCCCTGCTGCCAATCATGACCTAGACAAAGGGTTCCGGAAGGAGAACT
 GC~~AA~~**ATAGGAGGCCCTGGCTCCTGGCTGGCCAGCAGCTGCACTCTGTCTGTGCTC**
 CTCGGGGCATCCTGATGCTCCGGGCTCACCCCCCTCCAGCGGTGGTCCGGCTTCC
 GGAATTGGCCTGGCGTATGCAGAGGCCCTCACCCCCCTCCCCAGGGCTTGGTGGC
 AGCATAGCCCCACCCCTGCGGCCCTGTCACGGGTGGCCCTGCCACCCCTGGCACAA
 AAAATCCCACGTGATGCCATCATGCCCTCAGACCCCTTCTGGCTCTGCCGCTGGGGCTG
 AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAACTGGGTCAGCCTA
 GGGCAGGAGTCCCACCTCCAGGGCTCTGCTCGTCCGGGCTGGGAGATGTTCTGGAGGA
 GGACACTCCCATCAGAACTGGCAGCCTGAAAGTTGGGTCAGCCTCGCAGGAGTCCCAC
 CCTCTGGGGTGCCTGCCACCAAGAGCTCCCCACCTGTACCAACCATGTGGACTCCAG
 GCACCATCTGTTCTCCCAAGGGACCTGACTGAACTGGCAGCCCTGCTCCTCTGTGTTG
 CTTTGGGCCACCTGGGCTGACCCCTGCCCTTCTGCCCTACCCCTACCTAGCCTT
 CTCTCAGGCCACCTGATAGTCACGGCTCCCTGTGACTTCTGACCCCTGACACCCCTCC
 GGACTCTGCTGGCTGGAGTCTAGGGCTGGGGCTACATTGGCTTGTACTGGCTGAGGA
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 GCATCTGCTGGTGACCTGCCACCATCACAATAAGTCCCATCTGATTTAAAAAAAAAA
 AAAAAA

FIGURE 46

```
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PAYWDGEKEVLA VARGAPALLTCVNRGHVWTDRHVEEAQQVVHWDQPPGVPHDRADRLLDL
YASGERRAYGPLFLRDRVAVGADAFERGDFSLRIEPLLEVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEPPPGRGSPGNSSHSGAPGPDP TLARGHNVINVIVPESRAHFFQQLGYVLATL
LLFILLLVTLAARRRGGYEYSDQKSGKSKGDVNLA EFAVAAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPPLPAKYIDL DKGFRKENCK
```

Important features:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGGCGGCGTGGCGCAGCGGGCAGATGGCGTTGTCAGAGGACGACTT
 CAGCACAGTTAAACTCCACCTACGGAACACAAACGCCAGCAGTCAGCTCCGAGCTGACCAGGAGGC
 ACTGCTTGAGAACGCTGCTGGCACGGGCGGCGCTTGCGCATGGCCAGAGGCCAGGACCGCTTCT
 GTGGCACATACATCATCTTCTCAGCCGGCATGGCAGTCACTGGCATGGAACTCTT
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCCAACTCTCCAGGCCAGCCACCGGG
 GGACCTGAGGGCTCAGACATCTCTGAACACTTGTAGAGCTACCTTGGCGTTGCCTCCACCG
 TGCCCTCATGCTGTGCTGGCAACTCTCTGTGCTTGAACAGGGTTGCACTGGCAGTCACATC
 CGTGTCTGGCCTACTGACGGTCATCTGGCATCTTATGGTATAACTGCACTGGTGA
 GGTGGACACTCTCTGGACCCGTGGTTTTTGGCTCACCATTGTCATGGTATCC
 TCAGCGGTGCTTCACTGCTTCAGCAGCAGTCAGGGCATGACGGCTCTTTCTATG
 AGGAACCTCAAGCACTGATATCAGGAGGCCATGGGGGACGGTCAAGCCGGTGGCTC
 ATTGGTGGACTTGGCTGATCCAGTGATGTGAGGAACAGGCCCTGGCCTTCTTCTGAGG
 CCACCATCTCTCTGCTGCTGATGGGACTCACCTGCTGCTGGCTCAGGCTGGTATG
 AGGTAACATCATGAGGGCTTGTCTGGGGCATGGTGTGTTCTGGTGAAGAGGAGCTCCCCA
 GGACTCTCTCAGTGGCCCTCGTGGCTCCAGATTATGATTCCCACACCCCCCTC
 GCCCCATCTGAAGAAGACGGCAGGCCCTGGCTCTGTGTCACCTACGTCATCC
 AGCCTCATCACCCGGCCCTGCAACACATCAGGCTCTCAACAAGGGCTGGGCTACT
 GTGGACCAACCAAGTTTCTACCCCCCTCACTACCTTCTCTGTACAACTTTGTC
 GACCTATGTGGCCAGCTCACCGCTGGATCCAGGTGCCAGGGCCAACAGCAAGGCCCTCCAGG
 TTCGTGCTCTCCGGACCTGGCTCATCCCCCTCTCTGCTCTGTAAACTACCAAGCCCCGG
 CCACCTGAAGACTGTGGTCTTCCAGCTGGCAGTGTGACCTGGCAACTCTCAGGCTCTGG
 GGCTCAGCAACGGCTACCTCAGCACCTGGCCCTCTACGGGCTAAGATTGTGCCAGG
 GAGCTGGCTGAGGCCACGGGAGTGGTGTGCTTGTGCTGGGCTAACACTGG
 CTCAGCTGCTCATCCCCCTGGTGCACCTCATCAGTAGGGAGGAGCTGGTGA
 CTCAGAGCTTGTGAGATGAGAAGAGTGCAGGAGGGCTGGGGCATGGAGGAAGGCC
 TAAAGTTTCACTGGGACAGAGAGCAGAGCACACTCGGGCTCATCCCTCCAAGATGCC
 GTGAGGCCACCTCCATGCCATTCCGTGCAAGGCAGATATTCCAGTCATATTAA
 CAGAGAACACT
 CCTGAGACAGTTGAAGAAAATGCAAAATCAGGGTACTCCCTCACAGCTGATGGTT
 ACATTCCACCTTCTTCTAGCCCTCAAAGATGCTGCCAGTGTGTCGCCCTAGAGTTATTACA
 AAGCCAGTGCCAAAACCCAGCCATGGGCTTTGCAACCTCCAGCTGGCCTATTCCAGCT
 GACAGCGAGATGCAAGCAAATGCTCAGCTCTCTTACCTGAAGGGCTCTGGGAATGGA
 AGTCCCCCTGCGATGGTCAGTCAGCTCAGGCCAAAGACTCAACTGTGCA
 GACAGGCCCTGCTGCTGAGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCT
 GCGGGTGAACAACACTGCCACTAACAGAGCTGGAAAACCCAGAAAGATGGCC
 CTTCATCCAGAGGGACAGAGGGCTCCCTGTGCAAGGGATCAAGCATGTC
 GTGGCTGGGCTAAGATGAGGTCTTCAACATGTCAAGGCCATTGGTCA
 AGGGCTAATAATACTTGC
 GTATTAAAAA

FIGURE 48

MAVVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPGLQRPEDRFGTYIIFSLGI
GSLLPWNNFFITAKEYWMFKLNRSSSPATGEDPEGSDILNYFESYLAESTVPSMLCLVANFL
LVNRVAHVIRVLASLTVILAI FMVITALVKVDTSSWTRGFFAVTIVCMVIILSGASTVFSSSI
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY
LLLLSRLEYARRYMRPVLAAHVFSGEELPQDSLSAPSVASRFIDSHTPPLRPILKKTASLGF
CVTYVFFITSLIYPAVCTNIESLNKGSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP
GPNSKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL
LYGPKIVPRELAEATGVVMSFYVCLGLTGSACTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
305-330, 448-472

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FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCCGTGCCTGTCACCAAGAGCTGGAGACACCA
 TCTCCCACCGAGAGTC**ATGGCCCCATTGCCCTGCACCTCCTGTCCTCGTCCCCATCCTC**
 TCAGGCCCTGGCTCCCAAGGACTGGAAGGCTGAACGCAAGACCCCTTCGAGAAATGC
 ATGCAGGATCTGACTATGAGCAGCTGCTCAAGGTGGTACCTGGGGCTCAATCGGACCC
 GAAGCCCCAGGGTGATTGTGGCTGGTGTGCCGGGCTGGTGGCCGCAAGGTGC
 TCAGCGATCTGGACACAAGGTACCCATCTGGAGGCAGATAACAGGATCGGGGCCGATC
 TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCAG
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCTGGGCTCACCTGACCAAGTTCACCC
 AGTACGACAAGAACACGTGGACGGAGGTACGAAGTGAAGCTGCCAACTATGTGGTGGAG
 AAGGTGCCGAGAAGCTGGCTACGCCCTGCGTCCCCAGAAAAGGCCACTGCCCGAAGA
 CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACCTGGCTGAGAAAGG
 CGATGAAGAAGTTGAAAGGCACACGCTTGGAAATATCTCTCGGGGAGGGAAACCTGAGC
 CGGCCGGCGTGCAGCTCTGGAGACGTGATGTCCGAGGATGGCTTCTTATCTCAGCTT
 CGCCGAGGCCCTCGGGCCACAGCTGCCCTAGCGACAGACTCCAGTACAGCCGATCGTGG
 GTGGCTGGGACCTGTCGCCGCGCGTCTGAGCTCCGTGTCGGGCTTGTGCTGTTGAAC
 GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTCACGTGAGATCGAGACCTCTCC
 CCCGGCGCGGAATCTGAAGGTGTCGAAGGCCACGTGGTGTGTCGACGGCGAGCGGACCGG
 CGGTGAAGCGCATCACCTTCTGCCGCCGTGCCCGCACATGCAAGGAGGCCTGCCGGAGG
 CTGCACTACGTGCCGCCACCAAGGTGTTCTAACGCTCCGAGGCCCTCTGGCGCGAGGA
 GCACATTGAAGGCGGCCACTCAAAACCGATGCCGCGCATGATTTTCTACCCGCC
 CGCGCGAGGGCGCGCTGCTGGCCTCGTACACGTGGTGGACGCCGGCAGCGTTGCC
 GGCTTGAGCCGGGAAGAGGCGTTGCGCTTGGCGCTCGACGACGCTGGGGCATTGCA
 TGCGTGCGCCAGCTCTGGACGGCACGGCGTCGTCAGCGTGGGGAGGACAGCACA
 GCCAGGGTGGCTTGTGGTACAGCCGCCGGCTCTGCCAACCGAAAAGGATGACTGGACG
 GTCCCTTATGCCGCATCTACTTGCCGGAGCACCCCTACCCGCACGGCTGGTGGTGG
 GACGGCGGTCAAGTCGGCGCTGCCGCCATCAAGATCAACAGCCGAAGGGCTGCAT
 CGGACACGCCAGCCCGAGGGCACGCATCTGACATGGAGGGCAGGGCATGTGCATGGG
 GTGGGCCAGCAGGCCCTCGCATGACCTGGCAAAGGAAGAAGGCGACCCAGTCCAAGG
 CCAGTTATCTCCAAAACAGACCCACAGGAGCTGCAT**TAA**AGTATTTCGAAAAAA
 AA

FIGURE 50

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTWGLNRTLKPQRV
IVVGAGVAGLVAAKVLSDLAGHKVTILEADNRIGRIFTYRDQNTGWIIGELGAMRMPSSHRL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRYVVEKVPKEKLGYALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSEDGFFYLSFAEALR
AHSCLSDRQLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGPHDVHQIETSPPARNL
KVLKADVVLLTASGPRAVKRITFSPLPRHMQEALRRLYVPATKVFLSFRPFWRREHIEGG
HSNTDRPSRMIFYPPPREGALLASYTWSDAAAFAGLSREEALRLALDDVAALHGPVVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRUYFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEQGHVHGVAASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRTSH

Signal peptide:

amino acids 1-21

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FIGURE 51

CTGACATGGCCGTGACTGGGACAGCTCAGAGCAGGGCAGAAGCTGGGACACTCTGGCCGGCCTCTGCCTGCAT
 GGACGCTCTGAAGCCACCTGTCTGGAGAACACAGAGCGAGGGAAAGAGGACAGGGACTCGTGGCAGGAA
 GAACTCAGAGCGGGAGCCCCATTCACTAGAGACACTAGAGATCGGGCCCTCGCAGGGTCTGAATTCT
 GCTGCTGTCAAAAGATGCTTTTATCTTAACTTTTGTTCCTCCACTTCCGAGACAACTGACCTAACAGTTGCTG
 CTCGACATTGGAGCTGCCATCTCTGTGCTGTACCAAGACCTAACCCGTCTAACCTCTTGAACCTGAA
 CAATCAGTCTGTGGAAATTGAGGGAGGAGCACGGAAAGGGGTTTCCAGAAGAAACAATGACCTAACAGTTGCTG
 CTTCTCAGATGCCAAGACATGTAGTGGATTTCTTACAGATGCTATCTTACAAACAGGTGCTGTATAGAGCAGA
 ATATAGAAAACCACCGCCCTACAGATGCTATCTTACAAACAGGTGCTGTATAGAGCAGAATCTGGGTT
 CTGCTCTTGCTATAAGGTTATAAACATCACCGACCCCTGCGCATCTTGTGAGAATAGGGAGAGTG
 GATCATCTCGGATATTGGCTGTGATCACGTACTCTAGTGTACTCTGACCTCTGTGACACCTTGGGACCAAAGC
 CATCGTACATATTGTCAACAAGGCTGATATGCCATGGTATCTGTGACACACCCAAAAGGCATGGTGTGAT
 AGGGAAATGAGAAGAAAGGCTTCACCCGGACGGCTGAAAGGTGATCATCTTATGGACCCCTTGTATGACCTGAA
 CCAAGAGGGAGAACAGTGGAAATTGAGATCTTACCTTATATGATCTGAGAACCTTAGGAAAGAGCACTTCA
 AAAAGCTGTGGCTCAGGCCAAGAGCTGAGCTGATCTGTCACCCAGTGGGACCCACAGGTGACCCAAAAG
 AGCCATGATAACCCATCAAATATTGTTTAAAGTGTGCTGCTCTTCAAAATGTGAGGCTGACGACATGAGCC
 CACTCTGTGATGTGGCCATATCTCACCTCCCTGGGCTCATATGTTGAGGAGATTGTGACAGGCTGTTGTA
 CAGCTGTGGAGGAGGAGGATTTGGATTCAGGGTGTGCTGGCTGACGACATGAGAAGACTTGTGAGCC
 CACAGTGTCTCCGGCTCCTCGACTTCAACAGGATCTACGATAAGGTCACAAATGAGGCAAGACCCCT
 GAAGAAAGTCTGTGTAAGCTGCTTCCAGTAAAGTCAAGGCTTCAAAAGGGTATCATCAGGATGATAG
 TTTCTGGGACAGACTCATTTGCAAAAGATCCAGGACAGCAGCTGGGGAGGGTCTGTGTAAATTGTCAGTGGAC
 TGCCCCATGTCCTACAGTGTACCATCTCCGGGCAACATGGGATGTAGGTGATTAAGCCTATGGTCA
 AACAGAATGACAGGCTGGCTGTACATTACATTACCTGGGACTGACATCAGGTACGGTCACTGGGGTGGCCCTGG
 TTGCAATTACGTGAGCTGGAGAGTGGCTGACATGACTAACCTTACAGTGAATAATGAAGGAGGGTCTGAT
 CAAGGGTACAAACGTTCAAAGGATACCTGAGGACCCCTGAGAACAGACAGGGAGGCTGGACAGTGTGCTG
 GCTTACACAGGAGACATTGGTCTGGCTCGGAGCTGGAGATGGAAGCTGAGATCATGAGCTGGAAAGACATT
 CAAGCTGAGGAGGAGGAAATGAGCTGGGAGAGCTTACGGTACATCTTAGGTAGGGTGGTCTGTGACACAGATGACT
 ATTTCAGGCAAGCTGGGGTGAAGGCTCTTGTGAGGACTGTCAGGAAACCAAGGTGTAAGGGAGGCCATT
 AGAAGACTTGAGGAAATGGGAGAGCTTACGGTAAACAGGAGTCAACAGGAGTCAACCCAGTGTGTTTCTTC
 AGAGGCAATTTCATTTGCAAAATGGGAGGAGCTTCTCTTGTGTTTGTGATAAACATACCTTCAACAGGAGCT
 TGCACTGCTGTGAGAAAATGGTAAATTAAACTATTTCTTACATTGTTGCTTCTCTTATTTTTAAAC
 TGTTAAACTCTAAAGCCATAGCTTGTGTTTATATGAGACATATAATGTTGTAACCTAGTGTCCAAATAAATCA
 ATCCCTGCTTCCCACTCTCGATGTTGCTTCTCTTGTGCTGATCTTACACATGCTGCTTCAA
 GATCCCAGTTATGTTCTGTGCTTCTCTTGTGATCTTCAACCTTAAACTTATGAGTAAACCAACAGTCTCAAGGGT
 CAAAGGGAGCCCTGTGCTTCTCTTGTGTTTGTGATAAACATACCTTCAACAGGAGCTTCTCTATGCTT
 TCTTCAACTGTGTTCAAACTAAGAGATTAAATCTGAAACACTGCTACAACTCATGTTTCTGACCTCTCAC
 AAACCACTAAATTAGTTAGTTAGCTTACACTCATGTCATCATCTATGAGACAAATGTCGGAGCTGCTT
 CTGGCTAAATTAAATGGTACTGAGGGAAAGGGTGTGATCATACCAACATTTCTAAACTCTCTAGTGTG
 TCTGACTTGGGAGTAAATTAAATGGTCTATGACATACTGTCACAGGAAATGCTGTTCTAAAGCATTA
 CAGTAGGAAACTGGGAGGTAATCTGTTCTTACAGTTGGTGTGAGCTGGAAACTGTGGGGAGGGAGTTGACA
 GGTGGGCCAGTGAACCTTCCAGTAATGAAGCAAGCACTGATAAAGGAAACCTCTGAACCTGGGACAAAGATCT
 ACAGGCAAGCAAGATGCCACACAAACAGGCTTATTCTGTGAGGAAACACTGATCTCCCCACCCCTGGATT
 AGAGTTCTGCTACCTTACCCACAGATAACACATGTGTTCTACTGTAAAGCTTAAATGTTAAATTA
 TATTACAGAAAAAA

FIGURE 52

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775
<subunit 1 of 1, 739 aa, 1 stop
<MW: 82263, pI: 7.55, NX(S/T): 3
MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFN
FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPLLDLNNSQVGIEGGARKGVSKNNDLTS
CCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQPYRWSYKQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPWEWISELACYTYSMVAVPLYDTLGPEAIVHVNKAIDIAMVICDTPQKAL
VLIGNVEKGFTPSLKVIIIMDPFDLKRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIVSNAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQ
AVVYSCGARVGFQGDIRLLADDMKTLKPTLFFAVPRLLRNRIYDKVQNEAKTPLKKFLLKLA
VSSKFKELOQKGIIRHDSFWDKLIFAKIQDSLGGRRVRVITGAAPMSTSVMFFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHGVGPACNYVKLEDVADMNYFTVNEGEVCIKGTNVFK
GYLKDPKETQEAQALDSGWLHTGDIGRWPNGTLKIIDRKKNIFKLAQGEYIAPEKIEINIYNR
SQPVLQIFVHGESLRSSLVGVVVPTDVLPSSFAAKLGVKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPFSIENGLLTPTLAKRGELSXYFRTQIDSPLYEHIQD
```

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGGCGGAGGCCGCGGCAGCCGGGCCAGCAGTGAAGGGCCCTAGCGGGGCCAGCGGGG
 CCCGGGCCCCATAAGCCATCTCGAAGTCATGGCCTGCCAGACATTGTGACCGCCAAT
 CGGT**A**TGGACGACTGGAAAGCCCAGCCCCATCAAGGCCCTTGGGCTCGGAAGAAGCG
 AGCTGGTACCTACCTGAAGTATAAACCTGACAACCCAGCGGGCCCTCGGAGATTCTGTCA
 GACAGGGGCCGTCTTCTGTGGTACTGTCAATTGTCATAATCAAGTTGATCTGGACA
 CTCGCGAGCCCCATCAGTGAAAGCCAGAGGCCAGAGCAAGACTATGATGAGGCC
 CTAGGCCGCTGGAGCCCCACCGGCCAGAGGACTGGTCCCCGGGCTCTGGACGTAGA
 GGTGATTCAAGTCGACCAAAGTATATGTCAGTGGATGGCACACGGTCTGGAGGATG
 AGGCCGGGAGCAGGGGGCATCCATGTCAATTGTCCTCAACCAGGCCACGGGCCACGTG
 ATGGCAAAACGTGTTGACGACTCACCTCATGAGGATGAGGCCATGGTGTATTCT
 CAACATGGTAGCGCCCGGGCAGTCATCTGCACTGTCAAGGATGAGGGCTCTTCCACC
 TCAAGGACACAGCAAGGCTCTGTGAGGAGCCTGGCAGCCAGGCTGGCCCTGCCCTGGC
 TGAGGGACACATGGCTCTGGAGCAAAGGAGGCTCTGTCTGGGGAAACATTC
 TAAGTCACCTGCCCTCTCTCTGGGGGACCAACTCTGTGAGAGACAGATGTGCCATTGA
 GCTCAGCAGAAGAGGCAGACTGCCACTGGCAGACACAGACTGAACCGTCGCCCGGCC
 TTCTGCAGCAAAAGTTGAGGGCTATGAAAGTGTATGCAAGCTGAAGGACCCCACACCATCGA
 GTTCAGCCCTGACCCACTCCAGAACAAAGGCTCTCAATGTCCTGTGGCTGTATTGAG
 GGAACCGACCAAAATTACCTGTACAGGATGCTGCCCTCTCTTCAAGCCAGGGGTGTCT
 CCTCAGATGATAACAGTTCTTGATGAGGCTACTATGAGGAACCCATGGATGTGGTGC
 ACTGTGGTCTGAGGGCATCCAGCATACTCCATCAGCATCAAGAATGCCCGCGTCTCGC
 ACTACAAGGGCAGCCTACTGCCACTTCAACCTGTTGGGATTTTCAGTTCTGAGCCAATCCACCT
 CTGGAAGAGGACCTGGACATGCTGTGGATTTTCAGTTCTGAGCCAATCCACCT
 ACTGGAGGAGGATGACAGCTGTACTGCACTCTGCTGGAAATGACCAAGGGGTATGAAACACA
 CGGTGAGGGACCCAGCAGCAGTGTACCGCTGTGGAGACATGCTGGCTGGCTGGTGTCT
 AGGAGGTCTTGTACAAGGGAGGACTGGAGGCCAGTGGCTCAACCGAAAAGCTTGG
 TTGGGACATGGATGCCGATGCCGAACAACGCCGGGGAGAGTCATCATCCCTGACG
 TTCTCGATCTTCAACTTGTGGATCTGGCTGGCCTCAACATGAATGGTACTTTCTCAGGGC
 TACTTCAGAAGGACACAAGTCAACAGGGTCAAGGTGTCAGCTCAGGAAATGTGGACAGTCT
 GAAGAAAAGAAGCTTATGAAGTGGAAAGTTCAGGCTGCTAGTGAAGGCTGGGCTGG
 ACACAGAAGAACCTTGTGAAGACTTCTCTGGAGCACACAGAGGGCCACACCTAGCTGG
 TTATTCAGATGGAGAAAGATGACTCAACACCTGGACCCAGCTTGCACAGTCCCTCA
 TACTCGGACCTGGATGTCGGTGGCAACCATCGGGCCTGTGGAGATTGTTCTGGAAGAAA
 ACCACTTCTGTGGTGGGGTCCGGCTTCCCTACTCAGTGAAGAAGGCCACCCCTCAGTC
 ACCCCAAATTCTCTGGAGGCCACCCCAAAGGAGGAGGGAGGCCAGGACAGAC
 AT**TG**AGACCTTCCAGGACCTGCGGGCTGGGACTGTGTTGACCTCCAGGCTGGCTAGCC
 TCCCTCCATCTGTAGGATTGGTAGATGTCGGTAGGGCTGGGCTACCTTGTGTTAAC
 TGAGACTTAATTAACCTCAAGGGAGGGTTCCCTGCTCCAAACACCCCGTTCTGAGTT
 AAAAGCTTATTATTAACCTCTGGAGAAGGGCAGAGGAGTACCTGGGAATCATTACG
 ATCCCTAGCACTCATCTGGCTTGAATACCCACTCTTCCAGGGCTGGCTCAAGAATCTA
 ACCTATTATTAATGACTGTCTGAGGGCTTGAAAACAGGCCAACCTGGAGGGCTGGATTTC
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGCTGGCTTACTCAGGAAAATCTGTTG
 CAACCCATGAGCACAGGCCAGCTGGGCCACATGCTGACACAGACTCACTCAGAGAC
 GACACTGGACCAAGGCCCTCTCAGCCTCTCTGGAGGAAAGCTGGATAAGT
 GGTATTGATTTAAAAAGGAGAAGCCCTGGGAAAAAAAAAAAAAA

FIGURE 54

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQRALRRFCQTGAVLFLLVTIVNIKLILDTR
RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVVAVDGTTCVLEDEA
REQGRGIHVIVLNQATGHVMAKRVDFTYSFHEDEAMVLFNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSILGSQAGPALGWRDTWFVGRKGGPVFGEKHKSCKPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRLLLLRCSKVEGYGSVCSCDKPTIEFSPDPLPDNKVLNVPAVIAGN
RPNLYLYRMLRSLLSAQGVSPQMITVFIDGYEEMDVVALFGLRGIQHTPIISIKNARVSQHY
KASLTATFNIFPEAKFAVVLLEEDLIAVDFFSFLSQSIHLLLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRRLSLYKEELEPKWPTEPEKLWDWDMWMRMPEQRRGRECIIPDVS
RSYHFHGIVGLNMNGYFHEAYFKKKHKFNTVPGVQLRNVDSDLKKEAYEVHRLLSEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLVRGNHRGLWRLFRKKNH
FLVVGVVPASPYSVKKPPSVTPFILEPPPKEEGAPGAPEQT
```

Important features of the protein:

Transmembrane domain:

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

FIGURE 55

CGGACGCCTGGCTGCTGGGGAAAGGCCCTAAAGAAGTGGAAAGCCCACACTCTTGAACCAACAC
 CTGTAAAGAACCTAACCCATTAAAGGCCACTGGAAATTTGTTCTAGTGGTTGTGGGTGAATA
 AAGGAGGGCAGA**ATGGAT**TTCATCTCCATTAGCTGCTCTGGCTATGTGGTGGGATGTTA
 CGTGGCGGAATCATTCCCTGGCTGTTAATTCAGAGGAACGACTGAAGCTGGACTGTTGG
 GTGCTGGCCTTCCTGTGGAACTGCTCTGGCAGTCAGCTGGCTGAAGGAATGACATGCCCTTATGAA
 GATATTCTGAGGGAAAACACCCACCAAGCACTGAACACATAATGTGATTGATGCA
 AGACAAAGCAG
 AGAAAAATCAGTTGTCATGAACATGAGCACAGCACGACACACAGCTGATGCCCTATATTGGT
 TTTCCCTGCTGCTGGCTCTGGTCTGGTGGACCCAGATGGTAACCTCCATGTCATCT
 ACTCATGATTCACAACAGCACGCTAGCAACATACCCACAGCTGGCTGGGTTGTC
 TGCTGAGCTGATGGTGTGCTTGGGACACCACATCTACAGACCCAGTGTCCAGTTAATTG
 TGTGTTGGCAATCTGCTACATAAGGCCACAGCTGCTTGGGACTGGTTCCCTCTTGATGCTAGCT
 GCCCTTAGGCCAATGCAATCAGAAAGCCTTACAGAGGTGAACCCACGGGACTGG
 GGTGACACATACTTAGGACTGAGTAAGAGCAGTAAGAGCCTTACAGAGGTGAACCCACGGGACTGG
 CCATGCTTCTCTGCCCCGACATTCTTATGGTCCACAGTATGTCCTCCCTGAGGGGGGG
 ATAGGGCACAGCACAACGCCATGCCACGGGAGGGCTCAGCCGGCTGGAAAGTGGCAGCCCT
 GGTTCTGGGTTCCCTCATCCCTCATCTGCTAGTAGGACACCAGCAT**TA**ATGTTCAAGGTCAGC
 CTGGGTCAGGCCGCTGGCATCAGTGAAGAACACCCGGCACGTCAGCTACTCTCAGTC
 TCTGTCACCTGGCAGTCATCATGTATCCCTAGTGGGAGGGGGAGGTGAGGTTAACCTG
 ACTAATGAAAAGCTTTAGAGTAAAGAACATTTACAGTTCAGTTAGCTATAGACATCCCATGTT
 TATCTTAAAGGCCCTTGACATTCTGGCTTTAAATTCTCTTAACCTTACAGGGAAGATG
 GAATTAGTTTAAGGAAAAGGAGGAACACTCATACTCACATGAAATAGTGAATTATGAAAATACAGT
 GTTCTGTAATTAGCTATGCTCTTCTCTAGTTAGGGCTCTGCTACTTATCATTGATT
 AACATGTTCCACCATGTAAGACTGGTGTCTTAGCATCTGGCACATCGGTTGATGGAAGGTCTA
 GCACCCACTACTTAGATGCTAAAGGTGATCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATGAGC
 AAGACACATGAAAGCTCTTTATCTCAAAAGAGATATCCATTGAAAGGGATGCTAGAGGGATT
 TAAACAGCTCTTGGCACCGCCCTCTGATCAGCTGGCCTTCCATCAAATGGACAGGAGGAGG
 TGGAGGAGCTCTAAAGGGTAGCTTGTGTTAGCTTGTGATCTTGTCAAGTCTCCTTGGAGAAT
 ACCTGTCACCATCCCTAGAGGAGGCCAGTTCTAGTAGTTCTAGTTCTAGGCTTCTCAAGAA
 CAGTCAGATCCTAAAGGACTGCTTGGGAAATTAAAGGAGTATTAATTTAACTGATTTTGATGTT
 TGATATCTTGTAGCTTTTAAAGACTACCAAAAGTATGGTTCTCTTGTGTT
 TTTTTTTAAATTATTCTCTAGCAGATCAGCAATCCCTAGGGACCTAAATACTAGGTAGCTT
 GGCGACACTGTCTCTCACATAACCCCTGAGCAAGGGATCATAAAATGAGAAGTGTGCT
 TTGATTAAACCTATTGGAACTATGTCCTGCTCTGCTTCTGGTTCTTCTCAACTT
 TCCCTCTAGCTCTCTGCCACAATTGCTGCTACTGCTGGTTAATATTGTTGGGATGAAATT
 CTTATCAGGACAACCAACTCTCGAACCTGTAATAATGAGATAATAATCTTTATTCTTATCCCTT
 CAAAGAAAATTACCTTGTGCAAAATGCCCTTGTGGCCTTAAATACCCCTCTCATGTA
 ATTGACACAATCCTAAATCTGTAATTAAACAAATTGAGATAGCAGAAAGTGTAAACAGACTAGGATA
 ATTCTTCTTCAATTGGCAAAATTGGTAAACCCCTGCTCTGCAATAAATGTTAAATTGTT
 TATTAAATTATTACTCTCATACCTTCAAAACACATCAACTAAAGGGGAACCAAGAGTAGTT
 TCTTCAGGGCAGTGACGCTAGTAGTTGTAAGGAGCTTCTGACGCTAAAGCTAGCATGCCCTATG
 ATTATTTCTCTCATGAATTGGCACTGGGATCAGCAGCTGGAAATAAGCTTGTGAGGCCCTGCT
 GCCCACAGTGGGAAAGTACCAAAATGGATCAGTTCTATGCTAGTCAATTGGCAACAAATTG
 ATTTACTACCAAGAGAAGGTATGTTGAAAGTCCAAATGACTTCTCTGATTGGATGTTAACAGCT
 GACTGGTGTGAGACTTGAGGTTCTAGTCTGCTTCAAAACTATATGTTGGCTAGATTCTCTGG
 AACTGACTTTGCAAAATAGCAGATGTTAGTCAAAAAAA

FIGURE 56

MDDFISISSLISLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVHQ
IGNSHVHSTDDPEAARSSNSKITTLGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLLVFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPEVGGIGHSHKP DATGGRGLSRLEVAALVLGCLIP LILSVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

FIGURE 57

GCTCGAGGCCGGCGGCGGGAGAGCGACCCGGCGGCCCTCGTAGCGGGGCCGGATCCC
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTGAG**ATGAT**GGGCTTGG
 GAAACGGGCCTCGCACCATGAAGTCGCCGCCCTCGTCTGGCCGCCCTGGTGGCCTGCATC
 ATCGTCTTGGCTTCAACTACTGGATTGCGAGCTCCCGAGCGTGGACCTCCAGACACGGAT
 CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGTGCAAGAGAGAGGCCGTGGAGCTGAAGA
 AGAACGAGTTCAGGGAGGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC
 CACAACCTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTGGTGA
 TAACATCACACAGGTGAGGAGGCTATCCAGTGTGCAAGACCAAGTAAAGACCCCTGCAGA
 GGAATTACGGCAGGCTGCAGCAGGATGTCCTCAGTTTCAAGAACAGACCAACCTGGG
 AGGAAGTCTCCTACGACCTGAGCAGTGCATCAATCAGATGAAGGGGTGAAGGAACAGTG
 TGAGGAGCGAATAGAACAGGGTACCAAAAAGGGAAATGAAGCTGTAGCTTCCAGAGACCTGA
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
 GCAGCAGGCCGCCACACACAGAGGTGCCACAAGGGAAACGTGCTTGGTAACAGCAA
 GTCCCAGACACCAGCCCCCAGTCCGAAGTGGTTGGATTCAAAGAGACAAGTTGAGAAG
 AGGAAACCAATGAGATCCAGGTGGTAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG
 CCAGGCCGGGAGCAGGTGGTAAGACAGACACCTGTAGGTGGAAGAGGCTTCGGGGAGCCGG
 AGAACTGGGCCAGACCCCCACAGGTGCAGGCTGCCCTGTCAAGTGAGCCAGGAAAATCCAGAGA
 TGGAGGGCCCTGAGCGAGACCAGCTTGTCACTCCCGACGGACAGGAGGAGGAGCAGGAAGCT
 GCCGGGGAAAGGGAGAAACCAAGCAGAAACTGAGAGGGAGAAGAGTGAACAAACATGGATGAAAA
 TGAAGCAGAACATCTGAGACAGACAAGCAAGCAGCCCTGCGAGGGAAATGACAGAAACATAGATG
 TTTTAATGTTGAAGATCAAAAAGAGACACCAATAATTACTTGATCAGCGTAAAAAGCGG
 AATCATACACTC**TGA**ATTGAACTGGAATCACATATTCACAACAGGGCGAAGAGATGACTA
 TAAAATGTTCATGAGGGACTGAATACTGAAAATCTGTGAAATGACTAAATAATGTACATCTGA

FIGURE 58

MMGLGNRGRSMKSPPVLAAALVACIIVLGFNYWIASSRSVDLQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLQYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNLERKFSDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNNDQRQQQLQALSEPQPRLQAAGLPHTEVPGKGNGVLGNSKSQT PAPSSEVVLDSKR
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQQLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRDTINLLDQREKRNHIL

Signal peptide:

amino acids 1-29

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FIGURE 59

FIGURE 60

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLLELTNHSSCQEPPPGPGSLPWGSQGKPGACW
MASRFSRVVVLVIDALRFDFAQPQHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ
VDPPTTQMQLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRVVFMGDDTWKDLF
PGAFSKAFFFPSFNVRDLDTVDNGILEHLYPTMDSGEWDVILIAHFLGVDHCGHKHGPHPEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMTTNGDHGGDSELEVSAAFLYSPAVFPST
PPEEPEVIPQVSLVPTLALLGLPIPGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQ
QVSRLFLHTYSAAATQDLQAKELHQLQNLFSKASADYQWLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAISPGFPFCPLLTPVAWGLVGAIA
YAGLLGTIELKLDLVLLGAVAAYSSFLPFLWKAWAGWGSKRPLATLFPIPGPVLLLLFRILA
VFFSDSFVVAEARATPFLLGSFILLLVVQVLHWEQQLPPKLLTMRPLGTSATTNPPRHNGAY
ALRLIGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPRRLRVLVSGASMVLP
RAVAGLAASCLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVQPQIYRHMQE
EFRGRLERTKSQGPLTVAAQLGSVYSAAMVTALTLLAFLLLLHAERISLVFLLLFLQSFL
LILHLLAAGIPVTTPGPTVWPQAVSAWALMATQTFYSTGHQPVFPAIHWAAFGVGPPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLWPFLESQGLRKRQQPPGNEADARVRPEEEEEP
LMEMRLRDAPQHYAALLQGLKYLFIGIQLACALAAASILRRHLMVWKVFAPKFIFEAVG
FIVSSVGLLLGLIALVMRVDGAVSSWFRQLFLAQQR
```

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070**Leucine zipper pattern.**

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCCGCTGCCGCCGTGCTGTTGCTCTGGCGGCCCTGGGACGGGAGTCCCTGT
 GTCTCTGGGGTTGCCTAAACCTGCAACATCACCTCTTATCCATCAACATGAAGA**ATGT**
 CCTACAATGGACTCCACCAGGGTCTCAAGGAGTTAAAGTTACTACACTGTGCAGTATT
 TCATCACAAATTGGCCCACAGAGGTGGCACTGACTACAGATGAGAAGTCATTCCTGTTGT
 CCTGACAGCTCCAGAGAAGTGAAGAGAAAATCCAGAACAGCTCCTGTTCCATGCAACAAA
 TATACTCCAATCTGAAGTAAACGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC
 CAGTGTGACCAACCACAGCTGGTGCACCTGGCTGGAGCGAACACTCTTACTGCGT
 ACACGTGGAGTCCTCGTCCCAGGGCCCCCTCGCGTGCTCAGCCTCTGAGAACAGTGTG
 CCAGGACTTGAAGATCAATCATCAGAGTTCAAGGCTAAATCATCTCTGGTATGTTTG
 CCCATATCTATTACCGTGTCTTCTGTGATGGCTATCCATCTACCGATATATCCA
 CGTGGCAAAGAGAACACCCAGCAAATTGATTTGATTTGAAATGAATTGACAAAA
 GATTCTTGTGCTGCTGAAAAAATCGTATTAACCTTATCACCTCAATATCTCGGATGAT
 TCTAAATTTCTCATCAGGATATGAGTTACTGGGAAAAGCAGTGATGTATCCAGCCTTAA
 TGATCCTCAGCCCAGCGGGAACCTGAGGGCCCTCAGGAGGAAGAGGAGGTGAAACATTAG
 GGTATGCTTCGCTTGTGAGGAAATTGGACTCTGAAGAAAACACGGAAGGTTACTCT
 CTCACCCAGAACAGACTCCCTCAGCAGAACATAACCCCGGATAAAACAGTCATTGAATATGA
 ATATGATGTCAGAACCACTGACATTGCGGGGCTGAAGAGCAGGAGCTCAGTTGCAGG
 AGGAGGTGCCCCACAGAACATTGGAGTCGAGGAGGAGGTGAGCTTGGCC
 CAAACGTTACAGTACTCATACACCCCTCAGCTCAAGACTTAGACCCCTGGCGCAGGAGCA
 CACAGACTCGGAGGAGGGCGGAGGAAGAGCCATCGACGACCCCTGGTGACTGGGATCCCC
 AAACGGCAGGCTGTGATTCCTCGCTGTCAGCTTCGACCCAGGATTCAAGAGGGCTGCGAG
 CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTCTATCTAGACTCTATGAGGAGCCGGC
 TCCAGACAGGCCACCGAGGAGAAAATGAAACCTATCTCATGCAATTCTGAGGAATGGGGGT
 TATATGTGCAAGATGGAAA**ACTG**GCCAACACTTCTTTGCTTTGTTCTGTGCAAAC
 AAGTGAGTCACCCCTTGATCCAGCCATAAAAGTACCTGGGATGAAAGAAGTTTCTCAGT
 TTGTCAGTGTGAGGAAATTACTTATTCCTTCTTCTATCTCATAGCACGTTGATTG
 GTTCATGCATGAGGCTCTTAACATGATGGTGGGCCCTGGAGTCAGGGCTGCCGGT
 TCTTCTATGCAGAGAACAGCTAATAATGTTGCCAGACTGGGTGAGAACATTATTACAGG
 TGGGTGT

FIGURE 62

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQQRVFKELKLLTLCISSSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQ
CARTLKDKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILLYGNEFD
KRFFVPAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVEKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPPDKTVIEYEYDVRTTDICAGPEEQELSL
QEEVSTQGTLLESAQALAVLGPQLQYSYTPQLQDLDPLAQEHTDSEEGPEEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGDLGEEGLLSRLYEEPAPDRPPGENETYLMQFMEEW
GLYVQMEM
```

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCCTGGCGGACGCCTGGCGGACGCCTGGGTCTCTGCCGGGAGACGCCAGCCTGCG
 TCTGCC**ATGGGGCTGGGTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACGCCCT**
 GATGCTGCCGTGAAGCCCCCGCAGGCCCTGGGGGCCAGATCATGGGGGCCACGAGG
 TGACCCCCCACTCCAGGCCCTACATGGCATCGTGCCTCGGGGCCAACATCACTGCGGA
 GGCTTCCTGCTCGAGGCCCTGGGTGGTCTCGGCCGCCACTGCTTCAGCCACAGAGACCT
 CCCCACTGGCTGGTGGTCTGGGCCACGTCTGAGTAACGCCAGCAGCAGCAG
 TGTTGGCATCGATGCTCTCACACGCACCCGACTACCCACCCATGACCCACGCCAACGAC
 ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGCTCTGGCCCTGCAGTGGGCTGCTGAGGCT
 GCCAGGGAGAAGGGCAGGCCACAGCGGGACACGGTGCGGGTGGCTGGCTGGCTGGGCT
 TCGTGTCTGACTTGAGGAGCTGCCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC
 CCGGACGTCTGAAACAGCTCTGGAAAGGCCACCTGACACTTACCATGCTCTGCACCCGAG
 TGGGGACGCCACAGACGGGCTCTGCTCGGCCGACTCCGGAGGGCCCTGGTGTGCAGGA
 ACCGGGCTCACGGCTCGTTCTTCCTCGGGCTCTGGTGCGGCCAACCCAAAGACCCCGAC
 GTGTACACGCAAGGTGCGCCCTTGTCGGCTGGATCTGGACGTGGTCCGGCGAGCAGTCC
 CCAGCCCCGGCCCTGCCTGGACCACAGGCCAGGAGAAGGCC**TGAGCCACAACCT**
 TCGGGCATGCAAATGAGATGGCCCTCCAGGCCCTGGAAATGTTCCGTGGCTGGGCCACGGG
 AAGGCTGATGTTCAAGGTTGGGTGGACGGGCAGCGTGGGCACACCCATTCCACATGCA
 AAGGGCAGAACGAAACCCAGTAAAATGTTAACTGACAAAAAAAAAAAAAGAAA

FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAQIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSAEPQQVFGIDALTTHPDYHPMTHANDIC
LLRLNNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLTLMCTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWC GDPKTPDVY
TQVSAFVAWIWDVVRRSSPQPGPLPGTTRPPGEAA
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Signal peptide:

amino acids 1-30

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FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCCGACTCCGAGCCTGACGCCGA
 CGCCTGCCCCGGCCGGCAT**TG**AGGCCGCTACCTGCTGCCGCTGCGCGCTGGCACGGTAG
 CAGGCGCCGCCGTGCTCAAGGACTATGTCACCGTGGGCTTGCCCCAGCAAGGCCACC
 ATCCCTGGGAAGACGGTCATCGTACGGGCCAACACAGGCATGGGAAGCAGACGCCCTT
 GGAACCTGCCAGGAGAGGAGGCAACATCATCTGGCCTGCCAGAGACATGGAGAAGTGTGAGG
 CGGCAGCAAAGGACATCCGCCGGAGACCTCAATCACCATGTCACGCCGCCACCTGGAC
 TTGGCTCCCTCAAGTCTATCCGAGAGTTGTCAGCAAAGATCATTAAGAGGAGGAGCGAGT
 GGACATTCTAATCAACAACCGCGGTGTGATGCCGTGCCCCACTGGACCACCGAGGACGGCT
 TCGAGATCAGTTGGCTTAACCACCTGGTCACTTCTTGTGACAAACTTGCTGCTGGAC
 AAGCTGAAAGCCTCAGCCCCCTCGCGATCATCACCTCTGTCCTGGCCATGTTGCTG
 GCACATAGACTTGTGAGCAGCTGAACTGGCAGACGAGGAAGTATAACACCAAAGGCCCTACT
 GCCAGAGCAAGCTGCCATCGTCTCTCACCAAGGAGCTGAGCCGGGCTGCAAGGCTCT
 GGTGTGACTGTCAACGCCCTGCAACCCGGCTGGCCAGAGCAGAGCTGGGAGACACACGGG
 CATCCATGGCTCCACCTTCTCCAGCACCAACTCGGGCCATCTCTGGCTGCTGGTCAAGA
 GCCCCGAGCTGGCCGCCAGCCCAGCACATACCTGGCGTGGCGAGGAAGTGGCGATGTT
 TCCGGAAAGTACTTCGATGGACTCAAACAGAAGGCCCGCCCGAGGCTGAGGATGAGGA
 GGTGGCCCGAGGCTTGGCTGAAAGTGCCTGGCTTAGAGGCTCCCTGTGA
 GGGAGCAGCCCCCTCCCGAGAT**AA**CCTGGAGCAGATTGAAAGCCAGGATGGCCCTCCAG
 ACCGAGGACAGCTGTCGCCATGCCCGAGCTGGCACTACCTGAGCCGGAGACCCAG
 GACTGGCGCCGCCATGCCCGAGTAGTTCTAGGGGCGGTGCTGCCAGTGACTGGC
 CTGCAAGGTGAGCACTGCCCGGGCTCTGGCTGGTTCCCTCTGCTCTGTCGCCAGAGGGAG
 AGGGGCCATCTGATGCTCCCTGGAAATCTAAACTGGAAATGGCCAGGAGGAAGGGGCTC
 TGTGCACTTGCAAGGCCACGTCAAGGAGAGCCAGCGGTGCTGCGGGAGGGTTCAAGGTG
 TCCGTGAAGACATGGCAAGTTGTCAGACACTGGTGGATTCTGGTCCCTGTGGACCT
 TGTGCATGCATGGCTCTGAGCCTGGTTCTCAGCAGTGAGATGCTCAGAATAACTG
 CTGTCCTCCATGATGGTGTGGTACAGCGAGCTGTTGCTGGCTATGGCATGGCTGTGCCGG
 GGTGTTGCTGAGGGCTTCTGTGCCAGAGGCCAGCCAGAGAGCAGGTGCAAGGTG
 GAGTTCAAGGCTCTGCACGGCATGGAGTGGGAACCCACCAAGCTGCTACAGGACACTGG
 TTGCTGGACTCCACCTCTCATCAATTCTCATGGTAGTCCAAACTGCAGACTCTCAAAC
 TTGCTCATTT

FIGURE 66

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIIEEEERVDILINN
AGVMRCPHWTTEDGFEMQFGVNHLGHFLITNLNLLDKLAKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSQVTVNALHPGVARTELGRHTIGHGSTF
SSTTLGPIFWLLVKSPELAQPSTYLAVAELADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSvreQPLPR
```

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTTCGCGAGCGCTGGC**ATG**TGGTCTGGGGCGCGGCTGGCGGCCTGCTGGCGGTGCTG
 GCGCTGGGACAGGAGACCCAGAAGGCTCGCGGCTCGGGGACACGTTCTCGGCCTGAC
 CAGCGTGGCGCCGCCCCCTGGCAGGCCGCGCTGCTGGGCTGCTGAGGGTACCTGC
 GCGGGGAGGAGGCGCGCTGCGGGACCTGACTAGATTCTACGACAAGGTAATTCTTCAT
 GAGGATTCAACAACCCCTGTGGCTAACCTCTGCTTGACATTACTCATCAAACGCGTGA
 GTCTGACTGGAGGAATGTGACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTGAGG
 ATGGCTATGAGAACGTTGAGGAGCAAGCTTCAAGGACTTGAGGGAGCAGCAAGG
 GCCCTGATGCGGCTGAGGACGTGTACATGCTCAATGTGAAAGGCCCTGGCCGAGGTGCTT
 TCAGAGAGTCAGTGGCTCGCATCACTGACCTGACAGCCCCAAACGGCTTTTCTCTCA
 CAGGGATGAGTCGTTCCAAGTGGCAAGGTGGCTATGACATGGGGATTATACCATGCC
 ATTCCATGGCTGGAGGGCTGCTAGTCTTCAGGACATCTACGGAGACTGGAAGACAGA
 GGATGAGGCAAGTCTAGAAGATGCCCTGGATCACTGGCTTGCCTTGCCTTGCCTTGC
 ATGGTCTGTCGCCCCCTCTGGAGGACTTCTCTACAGCCCAGATAATAAGAGG
 ATGGCCAGGAATGTCATGGAAATATGAAAGGCTCTTGGAGAGGCCAACAGTGGTAGC
 TGAGGGCTGTCATCCAGAGGCCAATATACCCACCTGCAGACAGAGACACTACGAGGGC
 TATGTCAGACCTGGGTTCCAGCCACTCTCACAGATCCCTAGCTCTACTGTTCTAT
 GAGACAATTCCACGCCACTCTGCTCCAGGCCACTCCAGGAGGCTCATCCACCTGAA
 CCAGCATTGCTGCCCTCACAGGCCCTGGCTGCTCCAGGCCACTCCAGGAGGCTCATCC
 TGCTGACTATGGCATCGGAGGACACTATGAGCCTACTTGACCAGTGTACGTACCAAGC
 AGCCCCCTCTACAGAACATGAAGTCAGGAACCCAGGAGTTGCAACATTATGATCTATCTGAGCTC
 GGTGGAAAGCTGGAGGAGGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGTTAGGA
 ATGCGACAGTCTTGTGGAACCTGCACAGGAGTGTGTAAGGGGACAGTGACACACTCAT
 GCTGGCTGTCCTGTCCTGGGGAGATAAGTGGGTGGCCAAACAAGTGGATACTGAGATATGG
 ACAGGAATTCCGCAGACGCCCTGCAAGCTCCAGGCCCTGAAGA**ACTG**
 TGGTGAAGTCTGTGGCTTCCAGAGAACGCCAGGAGGAAAGCTGGGTAGGGAGGAGAAGC
 AGCAGAGCAGCCTCTGGAGAGAACGCCCTGTGCACTGGCTCTGCTGCTCGCAATCAGAGG
 AAGGGAGAGGTTGTTACCAAGGGGACACTGAGAATGTACATTGATCTGCCCCAGCCACGGAA
 GTCAAGAGTGGATGCACAGTACAAAGGAGGGGGAGTGGAGGCCCTGAGAGGAAGTTCTGG
 AGTTCAGATACTCTGTGGGAACAGGACATCTCACAGTCTCAGGTTGATCAGTGGTC
 TTTGGCACTTGAACCTTGACCAAGGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG
 GGGCTAGGCTGACTCCAGAACCTTAAAGACTTCTCCCCACTGCCTCTGCTGCAGGCCAAG
 CAGGGAGTGTCCCCCTCCAGAACATCCAGATGAGTGGTACATTATATAAGGATT
 TTTAAGTTGAAAACAACCTTCTTTCTTTGTATGATGGTTTTAACACAGTCATTTAAAA
 ATGTTATAAATCAAAA

FIGURE 68

MGP GARLA ALLA VLA LAL GTGD PERAA ARG DTF SALT SVAR ALA PERR LLG LL RRY LR GEE ARL
RDL TRFYD KVSL LHED STTPVANPLLAFT LIKRL QSD WRN VVHS LEASE NI RALK DGY EK VE
QDL PAFED LEGA ARAL MRL QDV YML NVKG LARG V FQR VTGS AITD LYSP KRL FSL TGDD CFQ
VGKV AYDM GDYY HAI PWLE AVS LFRG SYGEW KTE DEAS LED ALD HLA FAY FRAG NVSC ALS
LSREF LLYSP DNKR MARNV LKY ERLLA E SPN HVVA EAVI QRPN I PHL QTR DT YEG LC QT LGS
QPT LYQ I PSL YCS YET NSN AYLL QPI RKE VIH LEP YI ALY HDF VSD SEA QKIRE LAEP PWL Q
RSV VAS GEK QLQ VEY RISK SAW LKDT VDP KLV TL NHRIA ALT GLD VRPP YAEYL QV VNY GIG
GHY EPH FDHAT SPSS PLY RMK SG NR V AT FM IY LS SVE AGGATA F IY AN LS VP VVR NA ALF FWW
NLH RS GEG DSD T L HAG CPV LVG DKW VANK WI HEY GQ E FRR PCSS SPED

Signal peptide:

amino acids 1-19

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FIGURE 69

GAGATAGGGAGTCTGGGTTAACGTCCTGCTCCATCAGGAGCCCCCTGCTCCCACCCCTAG
 GAAGGCCACCAAGACTCCACCGGTGCGGGCCAATCAGGTGGAATCGGCCCTGGCAGGGGGGC
 ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCTGAAACCCGCGGGGGAG
 CGCCCCAGGATGCCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTCTCCTACCTC
 TGGCTCAAGTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATGGGGCCCTGGCTCT
 GTCTGTGGGCATCTATCAGAGGTGAGCGCAGAAAATATAAAACCCCTGAAAGTGCCTTCC
 TGGCTCCAGCCATCATCCTCATCCTCTGGCGCTGATGTCATGGCTCCTTCATTGGT
 GTGCTGGCGTCCCTCCGTGACAACCTGTACCTCTCAAGCATTGATGTACATCCTGGGAT
 CTGCCTCATCATGGAGCTCATGGTGGCGTGGCTGACCTCCGGAAACAGACCATTG
 ACTTCCTGAACGACAACATTGAGAGGAATTGAGAAGTACTATGATGATCTGGACTTCAA
 AACATCATGGACTTTGTCAGAAAAAGTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG
 GAGCAAGAACATCAGTACACAGACTGCAGTGCCCTGGACCCCTGGCCTGTTGGGTGCCCTAC
 CCTGCTGCATCAGGAACACGACAGAAAGTGTCAACACCATGTGTGCTACAAAATATCGAC
 AAGGAGCGTTTCAGTGTGAGGATGTCATCTACGTGGGGGCTGCAACCAACGCCGTGATCAT
 CTGGTTCATGGACAACATACACCATCATGGCGTGCATCCTCTGGCATCCTGCTTCCCAGT
 TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC
 TCTGTCACTGATGGGCTCTGGGGCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG
 ATGCTGCTTGTCTACCCCAATTAGGGCCACGCTGCCATGGCAGCTCAACAAGGACCGTC
 TGGAATAGCACCTCTAGTCACATCGTGGGCTGGACAGGGCTGCCCTGCCCAC
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGCTGTGTAGGTCCCACGGCCTGCGCTC
 CCCAGGGAGCAGACCTGGGCTCCCTAAGAGGCTTCCCCGAGGAGCTCTGGATCTG
 GCCCACCTGGGCTGGGAACAAGGCCCTCTTCCAGGCTGGCTACAGGGGAGGGA
 GAGCCTGAGGCTGCTCAGGGCCATTTCATCTCTGGCAGTGCCTGGCGGTGGTATTCAA
 GGCAAGTTTGTAGCACCTGTAATTGGGAGGGAGTGTGCCCTGGGGCAGGAGGGAAGG
 GCATCTGGGAAGGGCAGGAGGGAAAGAGCTGTCATGCAGCCACGCCATGGCCAGGTTGGC
 CTCTTCTCAGCCTCCAGGTGCTTGAGGCCCTCTTGCAAGGGCGGCTGCTTCCCTGAGCCTA
 GTTTTTTTTACGTGATTTTGTAACATCATTGGTACAGATAACAGGAGTTCTGAC
 TAATCAAAGCTGGTATTCCCCGATGCTTATTCTGCCCCACCAGTTGTTAA
 TCAAAACAATAAAACATGTTGTTGTTTAAAAAA

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYWLKFSLIIYSTVFWLIGALVLSVGIVYAEVERQKYKTLESAFLAP
AIIILLLGVVMFMVSFIGVLASLRDNLYLLQAFMYILGICLIMELIGGVVALTFRNQTIDFL
NDNIRRGVIENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA
 CACCTGGGAAGATGGCCGGCCCGTGGACCTTCACCCTCTCTGTGGTTGCTGGCAGCCACC
 TTGATCCAAGGCCACCCCTCAGTCCCCTGCAGTTCTCATCCTCGGCCAAAAGTCATAAAGA
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCAACAGCATCCTGCAGCAGCTGCCCTGC
 TCAGTGCATGCCGGAAAAGCCAGCGGAGGCATCCCTGTGCTGGCAGCCTGGTGAACACC
 GTCCCTGAAGGCACATCATCTGGCTGAAGGTCACTCACAGCTAACATCCTCCAGTGCAGGTGAA
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAGATCCCCCTGGACATGGTGGCTGGATTCA
 ACACGCCCTGGTCAAGACCACATCGTGGAGTCCACATGACGACTGAGGCCAAGGCCACCATC
 CGCATGGACACCAGTGCAGTGGCCCCACCCGCCCTGGTCTCAGTGA
 CTGTGACTGTGCCACCAGCCA
 TGGGAGCCTGCGCATCCAACTGCTGTATAAGCTCCTCTGGTGAACGCCCTAGCTAACG
 AGGTCA
 TGAACCTCCTAGTGCCTGCCAATCTAGTGA
 AAAACAGCTGTGCCGTG
 ATCGAGGCTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCATTTC
 CCTCAGCATTGACCGTCTGGAGTTGACCTCTGTATCCTGCCATCAAGGGTACACCATTC
 AGCTTACCTGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC
 TCTGCAGCTCCCTGACAATGCCACCCCTGGACAACATCCCGTTCAGCCTCATCGTAGTCA
 GGACGTGGTGAAGCTGCAGTGGCTGCTGTCTCTCCAGAAGAATT
 CATGGTCTGGTGG
 ACTCTGTGCTTCTTGAGAGTGCCCATCGGCTGAAGTCAAGCATGGGCTGATCAATAAAAG
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTAAGATCCTAAC
 TCACTCAGGGACACTCCCAGTT
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCA
 ACTGATCGTGTGGAAGTGT
 TTTCCCTCCA
 GTGAAGCCCTCCGCCCTTGTCA
 ACCCTGGGATCGAAGCCAGCTGGCAGCTCGGAAGCTCAGTTTAC
 ACCAAAGGTGACCAACTTAACTCAACTGAAATAACATCAGCTCTGATCGGATCCAGCTGAT
 GAACTCTGGGATTGGCTGGTCCAACCTGATGTTCTGAAAAACATCATCA
 CTGAGATCATCC
 ACTCCATCCTGCTGCCAACAGAACATGGCAA
 ATTAAAGATCTGGGGTCCCAGTGT
 CATTGGTG
 AAGGCCTGGGATTGAGGAGCTGAGTCTCA
 ACTGACCAAGGATGCCCTTGCT
 TACTCC
 AGCCTCTTGTGAAACCCAGCTCCTGTCTCCAGTGA
 AGACTTGGATGGCAGCCATCAG
 GGAAGGCTGGTCCCAGCTGGAGTATGGGTGAGCT
 TATAGACCA
 ATGCCCTCTCTGCAAT
 CAATAAACACTTGCCCTGTGAAAAA

FIGURE 72

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLLSAM
REKPAGGIPLVGLSLVNTVLKHIWLKVITANILQLQVKPSANDQELLVKIPPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGFTRLVLSDCATSHGSIRIQLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL
GAKLLDSQGKVTKWFNNSAASLTMPFLDNIPFSLIVSQDVVKAAVAAVLSPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGIEASSEAQFYTKGDQLILNLNNSDRIQLMNNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSGVPVSLVKALGFEAAESSLTKDALVLT PASLWKPSSPVSQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAAC**ATG**GCAGCGCGTTGGCGGTTTGGTGTCTGTGACCATGGTGGTGGCGCTG
 CTCATCGTTGCGACGTTCCCTCAGCCTCTGCCAAAGAAAGAAGGAGATGGTGTATCTGA
 AAAGGTTAGTCTAGCTGATGGAATGGAACAAAGACCTGTAATAAGAATGAATGGAGACA
 AGTTCGCGCCTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
 CTCCAACCTGCGATAGACAGTGTGCTTGCAGGCAAGCTGATGAAGAATTCCAGATCTGGC
 AAACTCTCGCGATACTCCAGTCATTCAACCAACAGGATATTGGCCATGGTGGAGTTTG
 ATGAGGCTCTGATGTATTTCAGTCTGAAATCAGTCAACTTTCATCAACTTT
 CCTGCAAAAGGGAAACCCAACGGGTGATACATATGAGTTACAGGGTGGGGTTTCAGC
 TGAGCAGATTGCGCCCGAGACAACGATGCAATATTAGACTGATTAGACCCC
 CAAATTATGCGGTCCCTATGTTGGGATCTTGGCTTATTGGTGGACTTGTAT
 CTTCGAAGAAGTAATATGAAATTCTCTTAAATAAAACTGGATGGCCTTTCAGCTTGTG
 TTTTGTGCTTGCTATGACATCTGGTCAATGTGGAACCATATAAGAGGACCACCATATGCC
 ATAAGAACCCCCACGGGACATGTAATTATCCATGGAAGCAGTCAGGCCAGTTGTA
 GCTGAAACACACATTGTTCTGTTAATGTTGGAGTACCTTAGGAATGTTGCTTGT
 TGAAGCTGCTACCTGACATGGATATTGGAAGCGAAAGATAATGTTGCTGGTATTG
 GACTTGTGTTATTCTCAGTGGATCTCTTATTTAGTCTAAATATCATGGTAC
 CCATACAGCTTCTGATGAGT**AAA**AAAGGCCAGAGATATAGACACTGGAGTACTGGAA
 ATTGAAAAACGAAAATCGTGTGTTGAAAAGAAGAAATGCAACTCTGATATTGTATTAC
 CTCTTTTTCAAGTATTAAATGTTAATCATTTAACCAAAGAAGATGTTGAGTGCCTTA
 ACAAGCAATCCTCTGCAAAACTGAGCTTGTGAAATTATTCCTTAACTCTCTT
 CCCAGTGAACCTTATGGAACATTAAATTACTACAAATTAGTATATTATAAAATTGAAA
 CTACTACTTTGTTTAGTTAGAACAACAGCTAAACTACTTTAGTTACTTGGTCTCTGAT
 TTATGATTTGCTTATCAGGAAAGTGGGAAAGTGGCTGACAGGTGTTCCACATATGCC
 TGTTACAGATAACTACATTAGGAATTCTAGCTTAGCTTCTCATTTGTTGAGTGT
 ACTTTACGCGATCTTCTTTGAGTAGAGAATTATGTTGTCATGGTCTCTGAAAATG
 GAACACCACTCTCACAGCACACGCTAGCCCTCAGCAAGACAGTTGTTCTCTCTCT
 GCATATTCCACTCGCGCTCCAGCCTGAGTGTAGAGTGAGACTCTGTC
 TCTCTAAATACAGGATTATAATTCTGCTTAGTGTGTTACTACCTTGTTATTAGAAA
 GATTTAGGATTCATTCCATCTCTTAGTTCTTTAGGTGACCCATCTGTGATAAAAATA
 TAGCTTGTGCTAAATCAGTGTAACTTACATGGCTAAATGTTCTACAAATAGAGT
 TTGTCATTATTCCATTGTTAGCTTAAGAGAAAATAGCCTCAGTTAGAAAAGGACTCCCTGG
 CCAGGCGCAGTGACTTACGCCGTAACTCAGCACTTTGGGAGGCCAAGCGAGATCAC
 GAGGTGAGGAGTTGAGACCATCTGGCCACATGGTGAACCCGCTCTACTAAAATA
 AAAATTAGCTGGGTGTTGGCAGGAGGCTGAAATCCAGCTACACAGGAGGCTGAGGCAC
 GAGAATCACTGAACCTGAGGAGATGGAGGTTCACTGAGGCCAGATCACGCCACTGCACTCC
 AGCCTGGCACAGAGCGAGACTCCATCTAAAAAAAAAAAAAA

FIGURE 74

MAARWRFWCVSVTMVALLIVCDVPSASAQRKKEMVLSEKVSQLM
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTN
SDVFQMLNMNSAPTFINFFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDV
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALAFCVLAMTS
PHTGHVNYIHGSQAQFVAETHIVLLFNGGVTLGMVLLCEAATSDMDIGKR
VLFWSWMLSIFRSKYHGYPYSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

FIGURE 75

FIGURE 76

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFDGRLTFHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPSSRAAMWSGLFTHLTESWNNFKGGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLLIRNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLGLNLPHPYPSGPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLS
EMHPVDYYSSYTKNCRFTKKEIKNIRAFYYAMCAETDAMLGEIIILAHQLDLLQKTIVIY
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMPGIKAGLQVSNVVSLSVDIYPTMLDIAGIPL
PQNLSGYSLLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSQDGAS
ILPQLFDLSSDPDELTNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWQSIG
QNYNSVIANLRWHQDWQKEPRKYENAIQWLKTHMNPRAV
```

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCACTGAGAGGTCTGCC**ATG**
 GCCTCTCTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCTCTGGGGCTTTGGCACACT
 GGTGCCATGCTGCTCCCAGCTGGAAAACAAGTTCTATGTCGGTGCCAGCATTGTGACAG
 CAGTGGCTTCTCCAAGGGCTCTGGATGGAATGTCACACACAGCACAGGCATACCCAG
 TGTGACATCTATAGCACCCCTCTGGGCTGCCGCTGACATCCAGGCTGCCAGGGCATGAT
 GGTGACATCCAGTGCAATCTCCTCCCTGCCCTGCATTATCTCTGTGGTGGCATGAGATGCA
 CAGTCTTCTGCCAGGAATCCCGAGCCAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTC
 ATCCTTGGAGGCCTCTGGGATTCAATTCTGTGCGCTGGAATCTTCATGGGATCCTACGGG
 CTTCTACTCACCACTGGCCTGACGCATGAAATTGAGATTGGAGAGGCTCTTACTTGG
 GCATTATTTCTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTCTGCTCATCC
 CAGAGAAATCGCTCCAACCTACTACGATGCCCTACCAAGGCCAACCTCTGCCACAAGGAGCTC
 TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGT
 ATGTG**TGA**AGAACCAAGGGCCAGAGCTGGGGGTGGCTGGGTCTGTGAAAAAACAGTGGACAG
 CACCCCCGAGGGCCACAGGTGGAGGGACACTACCACGGATCGTGTGAGAAGGTGCTGCTGAGG
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGCTAGTGTAAACAGCATG
 CAGTTGAATTGCCAAGGATGCTCGCATGCCACCTTCTGTTTCTCACCTGCTGCTC
 CCCTGCCCTAACTCCCCAACCTCAACTGAAACCCATTCCCTTAAGCCAGGACTCAGAGG
 ATCCCTTGGCCCTCTGGTTACCTGGGACTCCATCCCAACCCACTAATCACATCCACTG
 ACTGACCCCTGTGATCAAAGACCCCTCTCTGGCTGAGGTTGGCTTAGCTATTGCTGG
 GGATGGGAAGGAGAACGAGCTGGCTTTGGGATTGCTCAACCTACTTCTCAAGCTTCCC
 TCCAAAGAAACTGATTGGCCCTGGAACCTCCATCCACCTGTTATGACTCCACAGTGTCC
 AGACTAATTGTGCATGAACTGAAATAAAACCATCCCTACGGTATCCAGGGACAGAAAGCAG
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTAAAAAAATA

FIGURE 78

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYILGLLGLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAQAMMVTSAAISLACIISVVMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPVAWNLLHGIILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQNRNRSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNNSYSLTGYV
```

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 79

GCACGTGCTGCTGCCATCAGCTGCTGAAGCTCC**ATGGT**GCCCCAGAATCTTCGCTCTGC
TTATGTGTCAGTCTGTCCTCCTCTTGTCAGGAAAGTCATCGCTCCCGCTGGCTCAG
ACCATGGCTGTGCCAGCGCACCCAGGTGAGGACAAGATCTAACCCCTGGAGCAG
TGCTGTTAACATGACGCCATCGTGTCCCTGAGCGAGACCCGCAATGGTCCCCCTGCAC
CTTCTGGCCCTGCTTGAGCTCTGCTGTCTGATTCTTGGCCATCACAAACGATTGGTGTG
TGAAGCTGAAGGTTAGGGTGTGAATTCCCAGTGCACACTATCTCCATCTCAGATAATGT
GAAAGCAGAGACGTTTCC**TGA**GAAGACATAGAAAATCAATTCACTAAGGCATC
TCAGAAACATAGGCTAAGGTAATATGTGTACCAAGTAGAGAAGGCCTGAGGAATTACAAAATG
ATGCAGCTCCAAGGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAATAAAGTGGTTTCTCAATGTACACACCTGAAAAA

Group	Mean	SD	Median	Range	N
Control	1.00	0.00	1.00	0.00-1.00	10
ADL	0.98	0.02	1.00	0.95-1.00	10
MMSE	0.98	0.02	1.00	0.95-1.00	10
DS	0.98	0.02	1.00	0.95-1.00	10
DS-ADL	0.98	0.02	1.00	0.95-1.00	10
DS-MMSE	0.98	0.02	1.00	0.95-1.00	10
DS-DS	0.98	0.02	1.00	0.95-1.00	10
DS-ADL-MMSE	0.98	0.02	1.00	0.95-1.00	10
DS-DS-ADL	0.98	0.02	1.00	0.95-1.00	10
DS-DS-MMSE	0.98	0.02	1.00	0.95-1.00	10
DS-DS-ADL-MMSE	0.98	0.02	1.00	0.95-1.00	10

FIGURE 80

MVPRIFAPAYVSVC~~LLL~~C~~PREVI~~A~~PAGSEPWL~~CQPAPRCGDKIYNPLEQCCYND~~AI~~VSLSE
TRQCGPPCTFWPCFELCCLDSFGLTNDFVVKLKVQGVNSQCHSSPISSKCESRRRF

Signal peptide:

amino acids 1-25

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FIGURE 81

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTGCCATT
TTCTGCATCTCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT
GATGCTGTGCCAGGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTT
GCTATGATGATGCCGTGTCGCCCTGGCAGGACCCAGACGTGTGAAAATGCACCTTCAGA
GTCTGCTTGAAGCAGTGTGCCCTGGACCTTCATGGTGAAGCTGATAAACCCAGAACTGCGA
CTCAGCCCGGACCTGGATGACAGGCTTGTGCCAGTGTCAAGCTAAATGGAACATCAGGGAA
CGATGACTCCTGGATTCTCCTGGGTGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA
TCTGGATGCTGAGTGGCTGTTGGGGCCAGAGAACACACACTCAACTGCCACTTCATT
CTGTGACCTGCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCCTCTAG
AATTCTGGACAGCATGAGATGCGTGTGATGGGGCCCAGGGACTCTGAACCCTCTGAT
GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGAACCCCTTCACCC
TCTGTGAGATTTCCATCATCTCAAGTTCTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTATGACTTTATAATGAAAA

FIGURE 82

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCD SARTSDDRLCRSVS

Signal peptide:

amino acids 1-24

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FIGURE 83

GGGGGCGGGGTGCTGGAGCACGGCCTGGGGCCGCCCGAGCGCTCACTCGCTCGACTCAG
 TCGCGGGAGGCTTCCCCGCGCCGGCGTCCCAGCCGCTCCCGGACAGAAGTCCCT
 GCGCGTCCGACGGCAG**A**T**G**GGCGTCCCCACGGCCCTGGAGGCCAGCTGGCGCTGGGG
 TCCCTGCTCTCGCTCTTCCTGGCTGGCTCCCTAGGTCCGGTGGCAGCCTTAAGGTCGC
 CACGCCGTATTCCCTGTATGTCTGTCCCAGGGGAGAACGTACCCCTCACCTGCAGGCTCT
 TGGGCCCTGTGGACAAAGGGCAGATGTGACCTCTACAAGACGTGGTACCGCAGCTCGAGG
 GGCAGGGTGCAGACCTGCTCAGAGGCCGGCCATCCGAACCTCACGTTCCAGGACCTTC
 CCTGCACCATTGGAGGCCACCAGGCTGCCAACACCAGCAGCACCTGCTCAGGCCACGGG
 TGGAGTCGGCTCCGACCATGGCAACTTCTCATCACCATGCGAACCTGACCTGCTG
 GATAGCGGCCCTACTGCTGCTGGTGGAGATCAGGCACCAACTCGGAGCACAGGGT
 CCATGGTGCATGGAGCTGAGGTGCAGACAGGAAAGATGACCATCAA**A**C**T**G**T**G**G**T
 ACCCATCCTCTCCCAAGGATAGTGAACACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCTGGTCTACAAGCAAAGGCAGGCAGC
 CTCCAACCGCGTGCCAGGAGCTGGTGGGATGGACAGCACATTCAAGGGATTGAAAACC
 CCGGTTTGAAGCCTCACCACTGCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG
 TCCTATGTGGCCAGCGGCAGCCTCTGAGTCTGGGCGGATCTGCTTTCGGAGGCCAGCAC
 CCCCTGTCTCTCCAGGGCCCGAGACGTCTTCTCCATCCCTGGACCCCTGTCCTGACT
 CTCCAAACTTGAGGTCA**T**A**G**CCACGCTGGGGACAGTGGCTGTTGCTGGCTGGCTGG
 GGCAGGTGCAATTGAGGCCAGGGCTGGCTCTGTGAGTGGCCTCTGGCTCGGCCCTGGTTC
 CCTCCCTCTGCTCTGGGTCAGATACTGTGACATCCCAAGGCCAGCCCTCAACCCCTC
 TGGATGCTACATGGGATCTGGACGGCTCAGCCCTGTTCAAGGATTGGGGTGTGAG
 ATTCTCCCTAGAGACCTGAAATTCACCAAGCTCACAGATGCCAATGACTTACATCTAAC
 GTCTCAGAACGTCAGGCCCTCAGCAGCTCTGTTCTGAGACATGAGCCTGGGATGTGGCA
 GCATCAGTGGACAAGATGGACACTGGGCACCCCTCCAGGCACAGACAGGGCACGGT
 GAGAGACTTCTCCCGTGGCGCTTGGCTCCCCGTTTGCCGAGGCTGCTCTCTGTC
 AGACTTCCCTTTGTACCAAGTGGCTCTGGGGCAGGCCCTGCCACTGGCCATGCC
 ACCTTCCCAAGCTGCCCTCAGCAGTTCTCTGAAGATCTGCAACAGGTTAAGTCAAT
 CTGGGCTTCCACTGCCCTGCAATTCCAGTCCCCAGAGCTTGGTGGTCCGAAACGGGAAGTAC
 ATATTGGGCATGGTGGCCCTCGTGAGCAAATGGTGTCTGGCAATCTGAGGCCAGGACAG
 ATGTTGCCCAACCAACTGGAGATGGTGTGAGGGAGGTGGGTGGGGCTCTGGGAAGGTGA
 GTGGAGGGGACCTGCCCTGG
 ATTGAAGGGTGCACACAATGTCTGCTCACCCACTGGGACACTTCTGAGTATGAAGCGGGAT
 GCTATTAAAAACTACATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 84

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTYWYRSSRGEVQTCSEERRPIRNLTQFDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLDSGLYCCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSQ
DSENITAAALATGACIVGILCLPLILLLVYKQRQAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPPGDVFVFFPSLDPPDSPNFEVI
```

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTCGTCTCCATCTCCCTCCT
 TTCCCCGCGTCTCTTCCACCTTCTCTTCCACCTTAGACCTCCCTCCGCCCTC
 TTTCTGCCAACCGCTGCTCTGGCCCTTCTCCGACCCGCTCTAGCAGCAGACCTCCCTGG
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCCTTTCGTCCTCCCTCCCGA
 CTCCGCTCCCGGACCAGCGGCCTGACCCGGAAAGGAATGGTTCCCGAGGTGAGGGTCTC
 TCCTCCTGCTGGACTCCGCTGCTGGTCCCCCTGGACTCCACGCTCGAGGCCGCC
 AGACATGTTCTGCCTTTCCATGGGAAGAGATACTCCCCCGCGAGAGCTGGCACCCCTACT
 TGGAGCCACAAGGCCTGATGTAECTGCCTGCCTGACTCTGCTCAGAGGGCGCCCATGTGAGT
 TGTTACCGCCTCCACTGTCCGCTGTCCTGCCCCAGCCTGTGACGGAGCCACAGCAATG
 CTGCTCCAACTGTGTGGAACCTCACACTCCCTGGACTCCGGCCACCAAAGTCTCTGCC
 AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCTC
 CGCCTGCCAACCCAGTGTGCTCTGCGACTGCACAGAGGGCAGATCTACTGCGGCCAC
 AACCTGCCCGAACCCAGGTGCCCAGCACCCCTCCACTGCCAGACTCTGCTGCCAAGGCC
 GCAGGAGATGAGGCAAGTGAAGCAATCGGATGAAAGAGGACAGTGTGCAGTCGCTCCATGGGTG
 AGACATCCTCAGGATCCATGTTCCAGTGTGATGCTGGGAGAAAGAGAGGGCCGGCACCCAGC
 CCCCACGGCTCAGGCCCTCTGAGCTTCATCCCTGCCACTTCAGACCCAAGGGAGCAG
 GCAGCACAACGTCAAGATGTCCTGAAGGAGAAACATAAGAAGCCTGTGTCATGGCGGG
 AAGACGTACTCCACGGGAGGTGTCGACCCGGCTTCCGTGCCTTCGGCCCTTGCCCTG
 CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCACCGAGT
 ACCCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCTGAAGATTGCCAGAGGACAAA
 GCAGACCCCTGCCACAGTGAGATCAGTTCTACCAAGGTGTCACGCCAGGACACGGGCGGGTCC
 CGTCCACACATCGGTATCCCCAAGCCAGACAACCTGCGTCGCTTGCCTGGAACACGAGG
 CCTCGGACTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAAACTGAGGCTCAG
 AGAGGTGAAGTACCTGCCAACGCCACAGCCAGAACTTCCACTGACTCAGATCAAGA
 AAGTCAGGAAGCAAGACTCCAGAAAGAGGGCACAGCACTCCGACTGCTCGTGGCCAC
 GAAGGTCACTGGAACGTCTCCAGGCCAGACCCCTGGAGCTGAAGGTACGCCAGTCCAGA
 CAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT
 ATTATATATTAATAAGAAGTGCATTACCTCAAAAAAAAAAAAAAA

FIGURE 86

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVEPVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTETPQQCCPKCVPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFPSRLPNQCVLCSCTEGQIYCGLTTCEPEPGCPAPLPLPDSCQACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKGPGTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTEYPCRHPEKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRALEHEASDLVIEYLWKLV
KDEEETEAQRGEVPGPRPHSQNLPLSDQESQEARNPERGTALPTARWPPRSLERLPSPDFG
AEGHGQSRQSDQDITKT
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Signal peptide:

amino acids 1-25

FIGURE 87

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGCAACAGCTTGC CGCTGC GGGGAGCTCCC
GTGGGCGCTCCGCTGGCTGTGCAGGC GGCA **ATGGATTCTTGC**GGAAAATGCTGATCTCAGT
CGCAATGCTGGCGCAGGGCTGGCGTGGCTACGCCTCCTCGTTATCGTGA CCCC GGGAG
AGCGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAAGGAGCAGGGAGGAG
GCGGCCAGGACCCAGCAGCTATTGCTGCCACTCTGCAGGAGGCAGC GACCACGCAGGAGAA
CGTGGCCTGGAGGAAGAAC TGGATGGTTGGCGCGAAGGCGGCGCCAGCGGAGGTCA CCGT
GAGACCGGACTTGCCTCCGTGGCGCCGACCTTGGCTTGGCGCAGGAATCCGAGGCAGCC
TTTCTCCTTCGTGGGCCAGCGGAGAGTCCGGACCGAGATA CCATGCCAGGACTCTCGGGG
TCCTGTGAGCTGCCGTGGGTGAGCACGTTCCCCAAACCTGGACTGACTGCTTAAGGT
CCGCAAGGCGGGCAGGGCGAGACGCAGTCGGATGTGGTGA ACTGAAAGAACCAATAAAA
TCATGTTCCCTCAA
AAAAAAAAAAA

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FIGURE 88

MDSLRKMLISVAMLGAGAGGVGYALLIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLATLQEAATTTOENVAWRKNWMVGEGGGASGRSP

Signal peptide:

amino acids 1-18

FIGURE 89

CAGGAGAGAAGGCACCGCCCCACCCGCCCTCAAAGCTAACCCCTGGGCTTGAGGGAAAGA
 GGCTGACTGTACGTTCTTCACTCTGGCACCACTCTCCAGGCTGCC**ATGGGGCCCAGCAC**
 CCTCTCCTCATCTTGTTCCTTGTATGGTCGGGACCCCTCCAAGGACAGCAGCACCCACCT
 TGTGGAGTACATGGAACGCCGACTAGCTGCTTAGAGGAACGGCTGCCAGTGCCAGGACC
 AGAGTAGTCGGCATGCTGAGCTGCCAGGACTCAAGAACAGATGCTGCCACTGCTGGAG
 GTGGCAGAGAAGGAGCGGGAGGCCTCAGAACACTGAGGCCACACCATCTGGGAGAGTGG
 TCGTCTGGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCCAGCTGCCCTGTAGAGT
 TTGATGAGAAGGTGACTGGAGGCCCTGGGACCAAGGCAAGGGAAAGAAGGAATGAGAAGTAC
 GATATGGTACAGACTGTGGCTACACAATCTCAAGTGGATCAATGAAGATTCTGAAGCG
 ATTTGGTGGCCAGCTGCTATGGACCAAGGATCCACTGGGCAAACAGAGAAGATCTACG
 TGTAGATGGGACACAGAACAGACAGCCTTGTCTTCCAAGGCTGCGTGACTTCACCCCT
 GCCATGGCTGCCCGAAAGCTCCCGAGTCGGGTGCCCTTCCCTGGTAGGCACAGGGCA
 GCTGGTATATGGTGGCTTCTTATTTGCTCGAGGGCTCTGGAAAGACCTGGTGGAGGTG
 GTGAGATGGAGAACACTTGCAGCTAACAAATTCCACCTGGCAAACCGAACAGTGGTGGAC
 AGCTCAGTATCCCAGCAGAGGGCTGATCCCCCTACGGCTTGACAGCAGACACCTACAT
 CGACCTGGTAGCTGATGAGGAAGGTCTTGGGTGTCATGCCACCCGGGAGGATGACAGGC
 ACTTGTGTCGGCAAGTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGACACACCCA
 TGTCCCAGAGAGAATGCTGAGGCTGCCCTTGTCATCTGGGACCCCTATGCTGCTATAA
 CACCGTCTGCCAGTCGGCCCGCATCCAGTGTCTTGTGCCAGCGGCCACCTGACCC
 CTGAACGGGCAGCACTCCCTATTTCCCGCAGATATGGTGCCATGCCAGCCTCGCTAT
 AACCCCCGAGAACGCCAGCTCATGCCCTGGATGATGGCTACCAAGATTGCTATAAGCTGGA
 GATGAGGAAGAAAGAGGGAGGTT**TGA**GGAGCTAGCCTGTTTGATCTTCTCACTC
 CCATACATTATATTATATCCCACTAAATTCTGTCCTCATTCTCAAATGTGGGCCAG
 TTGTCAGCTCAAATCCTATATTAGCCAATGGCAATCAAATTCTTCAGCTCCTTGTT
 TCATACGGAACTCCAGATCTGAGTAATCCTTTAGAGCCGAAGAGTCAAAACCCCAATG
 TTCCCTCCTGCTCTCCGTCCAGGCTCAACAAATTCTGAGGCTAAGGATGCCAGGCCAGG
 GCTCTAACCTGTATGCCAGGCCAGGGAGCAGGAGCAGCAGTGTCTCCCTCAGAGTG
 ACTTGGGAGGGAGAAATAGGAGGAGACGTCAGCTGTCCTCTCCCTCACTCCCT
 TCAGTGTCTGAGGAACAGGACTTCTCCACATTGTTTGATATTGCAACATTGCAATTAAA
 AGGAAAATCCACAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAA

FIGURE 90

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46038, pI: 6.50, NX(S/T): 2
MGPSTPLLILFLLSGPLQGQQHHLVEYMERRLAALLEERLAQCQDQSSRHAAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVVDLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDGYTISQVRSMKILKRGFGPAGLWTKDPLGQTEKIVLDGTQNDTAFVFPR
RDFTLAMAARKASRVRVFPFWVGTGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN
RTVVDSVFPVPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTEQ
QWDTPCPRENAEAAFVICGTLVYVNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPREROLYAWDDGYQIVYKLEMRKKEEEV
```

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

FIGURE 91

GACAGCTGTCTCGATGGAGTAGACTCTAGAACAGCGCAGTTGCCCTCCGCTCACGCAG
 AGCCTCTCGTGGCTTCGCCACCTTGAGCATTAGGCCAGTCTCCTCTCTAATCCAT
 CCGTCACCTCCTGTATCCGTTCCATGCCGTGAGGCCATTACAGAACACATCC**ATGG**
 CTCTCATGCTCAGTTGGTCTGAGTCTCCTCAAGCTGGATCAGGCCAGTGGCAGGTGTT
 GGGCCAGACAAGCCTGTCAAGGCCCTGGTGGGGAGGACGCAGCATTCTCTGTTCTGTC
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCCTTCTCAGGGCCAGTCTCTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTATGCAGATGCCACAGTATCAAGGCAGG
 ACAAAACTGGTGAAGGATTCTATTGGGAGGGCGCATCTCTGAGGCTGGAAAACATTAC
 TGTGTTGGATGCTGGCTCATGGTGCAGGATTAGTCCCAGTCTACTACCGAAGGCCA
 TCTGGGAGCTACAGGTGTCAGCACTGGCTCAGTCTCTCATTTCCATCACGGGATATGTT
 GATAGAGACATCCAGCTACTCTGTCACTCCTCGGCTGGTCCCCCGCCACAGCGAAGTG
 GAAAGGTCCAAGGACAGGATTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 TGGTGTGGAGATCTCTGACCGTCCAAGAGAACGCCGGAGCATATCCTGTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACTTTTCGA
 GCCTATATCGTGGCACCTGGTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTG
 GCATTGTTGACTGAAGATTCTCTCAAATTCCAGTGGAAAATCCAGGGGAACACTGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACCGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTACCCGAAGCTCGTTCTGATCTGAAAATGTAAACCCATA
 GAAAAGCTCCCAGGAGGTGCTCACTGTGAGAAGAGATTACAAGGAAGAGTGTGGTGGCT
 TCTCAGAGTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG
 GCGCGTGGGAGTGTGCCGGATGATGTGGACAGGGAGAAGGAGTACGTACTTGTCTCCG
 ATCATGGGTACTGGTCTCAGACTGAATGGAGAACATTGTATTCACATTAAATCCCGT
 TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTCTGGACTATGAGTG
 TGGGACCATCTCTTCTCAACATAATGACCGATCCCTTATTATACCTGACATGCGGT
 TTGAAAGGTTATTGAGGCCCTACATTGAGTATCGTCATAATGACCAAATGGAACCTCC
 ATAGTCATCTGCCAGTCACCCAGGAATCAGAGAAAGAGGCCCTTGGCAAAGGCCCTG
 AATCCAGAGACAAGCAACAGTGAGTCTCTCACAGGCAACCACGCCCTCCAGGG
 GTGAAATG**TAG**GATGAATCACATCCCACATTCTCTTGTAGGATATTAGGTCTCTCCCA
 GATCCAAAGTCCCGCAGCAGCCGCCAAGGTGGCTTCAGATGAAGGGGACTGGCCTGTCC
 ACATGGGAGTCAGGTGTATGGCTGCCCTGAGCTGGGAGGAAAGAAGGCTGACATTACATT
 AGTTGCTCTCACTCCATCTGGCTAAGTGATCTGAAATACCACCTCAGGTGAAGAACCG
 TCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTGTCATTATATTACACTTCAGTA
 AAAAAA

FIGURE 92

MALMLSIVSLLKLGSQWQVFGPDKPVQALVGEDAASFCLSPKTNAEAMEVRFFRGQFSS
VVHLYRDGKDQPFMQMPPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYYQK
AIWELQVSALGSVPLISITGYVDRDIQLCQSSGWFPRPTAKWKGPQGQDLSTDRTNRDMH
GLFDVEISLTQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFWQKIQAEQDWRRKHGQAEELRDAKHAEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS
PDHGywVRLNGEHLYFTLNPRFISVFPPRTPTKIGVFLDYECGTISFFNINDQSLIYTLC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAIPETSNSESSSQATTPFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGCGCCGGTGGCGGTGGCGCGTTGCGGAGGCTTCCTGGTCGATTGCA
 ACCAGGAGAAGATGACTGACCAACCAGTGGCTGAATGAATGCGGAGCCGAGCAGC
CATGAGGAGCCCTGCCGAGCCCTGGCGCCCTCGCGGGAAATGTCACCGGTGCGGGCGGGCCGCCCCGCG
 CCCGCGCTCAGCCGCCCTCGCGGGAAATGTCACCGGTGCGGGCGGGCCGCCCCGCG
 GACCGCTGCCGGGCCCGGGTTGCGGGCGAGCCCAGCACCCCTCCCTAGGGGACCGC
 TCCCCACGGCCCAGGGCCCCGAGGACGGGCCCGCGGCCACCGTCCACCGAACCCCTGGCTG
 CGACCTCTCCAGCCCCAGTCCCCGAGACCCCCCTTTGGCGACTGTGGACCTCTTCC
 ACCACCTTCAGGGCCGCTCGGCCCTCGCGGACCAACCCCTCCGGCGGGAAACGCAC
 GACCACTCTCAGGCGCCGACAGACCCCGGCCGACCAACCTTCGACGACCAACTGGCCG
 CGCCGACCAACCCCTGTAGCGACCCAGTACCGGCCAACGACTCCCCGGACCCCG
 GATCTCCCACAGCACGACCAACAGCAGCGCTCTCCCCAACCTGCCAACCGAGGGCC
 TTGCGCTCTCCAGAGTATGTAACTGCTGTGTTGAGCTGAATGTGAATCGT
 GCAACAGACACAGGGCATGTGAGTGTGGCCAGGTTACAGGGGCTTCACTGTGAA
 TCCAAAGAGGGCTTCTACCTAAATTACACTCTGGCTCTGTGACGCATGTGACTGTAGTCC
 ACATGGAGCTCTAGCATACCGTGAACAGG**TAAG**CAACAGAGGGTGAACACTGAAGTTATT
 TTATTTAGCAAGGGAAAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTAACAAAG
 GAGGATGAGGTCTCATAGATTACAAAATTTATTAACCTTCTTACTTTACTTATATGT
 TATATTAAATGTCAGGATTAAAAAACATCTAAATTACTGATTAGTCTCAAAGACTAG
 AGTCGCCATTTCCTGGATAATTCTGTAATTCTCATGGGAAAAATTATTGAGA
 AAATCTGCTCTGGCAAGGGCTTCAAGGATGAAACCTGCTAGGAGGTAGAAATGTTCTT
 ATGTTATTAAATACCATTTGGAGTTGAGGAAATTGGTTGTGTTGTTTATTCTCTCA
 ATCAAATCTACATTGTTCTTGACATCTAAAGCTAACCTGGGGTACCCCTAAATT
 TTTAACTAGGTAGACTGGTTTACTCTATTACAGTACATTGGAGACAAAAG
 TAGATTAAGCAGGAATTATCTTAAACTATTGTTATGGAGGTAATTAAATCTAGTGG
 ATAATGACTGTATCTAACGATTGGCTCTGTGACTGCACTGAAAGTAATTATTCTTGAC
 TATGTGAGGCACTGGTTTGTGGACCCAAGTCAAAAACTGAAGAGACAGTTAAAT
 AATAAAAAAATTAATGACAGTTACTCAGTGAACCTGGTATAACCCAAGAGTC
 CACTTACGAGCTGTGTTCTGGGCAAGTAATTCTTCTACTGAGCTGTTCTCTCAAG
 GTTGTGTGAAGATTAAATGAGTTGATATATAAAATGCCAGCACATGCACTCA
 TTCTGGTTTGTGTTAATTCAAGGAATTATGACTGAAATGAGAGAACATGTTTAAGA
 ACTTTAGCTCTTGACAAGAAGTCTTATCTTACCTTACGACTAAATATTAAATGTT
 TAAATGATATTAACTGTATGAAATTGATCATATTGACTTTATTAAATGAGAG
 AGGCTGGCGCGTGGCTACCCCTGTAATCTTAGCCTTGGGAGGCCAAGGCGGGTGGAT
 CACTTGAGGGCAGGAGTTCTAGATGAGCTGGCCAGCACAGTGAAACCCCGTCTACT
 AATACAAACAAATTAGCTGGCGTGTGGCACACACCTGTACTCCAGTACTCGGGAGG
 GAGGCAGGAGAATCGGTTGAACCCGGGGAGGTGGAGGTTGCACTGAGCTGAGA
 TCGCGCCACTGCACTCCAGGCTGGTGAAGAGAGGGAGACTCTGTCTTAAAAA
 AAAAAAAAAAAAAA

FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLPSLGGIALLCCAAAAAVASAASAGNVVTGGGAAGQVDASPGPGLRGEPSHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPLWATAGPSSTTFQAPLGSPPTTPAAERTS
TTSQAPTRPAPTTLSTTGPAAPTTEVATTVPAPTTPTPDLPSSNSSVLPTTPATEAPS
SPPPEYVCNCVVGSLNVNRCNQTTGQCERPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGCGGCAGTGTAGACCTGGGAGG**ATGGCGGCCCTGCTGGCTGCTTTCTGGCTTG**
TCTCGGTGCCCAAGGGCCCAGGCCGTGTGGTGGGAAGACTGGACCTGAGCAGCTTCTGGG
CCCTGGTACCGTCTGGCTGGCCTCCGGAAAAGGGCTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGGTGGTGGTGAACCTCACTCCAGAAAACAACCTGCGGACGCTGTCCCTCTC
AGCACGGGCTGGAGGGTGTGACCAGAGTGTCAAGGACCTGATAAAAGCGAAACTCCGGATGG
GTGTTTGAGAACCTCAATTAGGCGTGTGGAGCTGGGTGCTGGCACCAACTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTGGGGACGAGCCCTAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGTCTTCACCAAGTGGAGCAGGAGC
CTGGGCTTCTGTCAAG**TAGCAGGCCAGCTGCAGAAGGACCTCACCTGTGCTACAAGAT**
CCTCTGTGACTGCTGCGTCCCCAGTAGGGATGCCGCCACAGGGTCTGTGACCTGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCGGGGCCAGCACCAGCTCAGAATAAAAGCGATT
CACAGCA

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FIGURE 96

MGGLLLAAFLALVSVPRAQAVWLGRDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT
LTPENNLRITLSSQHGLGGCDQSVMIDLKRNSGWVFENPSIGVLELWVLATNFRDYAIIFTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

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FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTTAACCCCAGACATGCCTGCTGCTGCTGCC
 CCTGCTCTGGGGGAGGGAGGGCGGAAGGCAGACAAGTAAACTGCTGACGATGCAGAGTT
 CCGTGACGGTCAGGAAGGCCGTGTCATGCCATGCCCTGCCCTCCTACCCCTCGCAT
 GGCTGGATTACCCCTGCCAGTAGTCATGCCACTGGTCCGGGAAGGGGCCAACAGA
 CCAGGATGCTCCAGTGGCACAAACAACCCAGCTGGCAGTGTGGAGGAGACTGGGACC
 GATTCCACCTCCTGGGACCCACATAACAAGAATTGACCCCTGAGCATCAGAGATGCCAGA
 AGAAGTGATGCCGGGAGATACTTCTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATCACCGGCTCTGTGAATGTGACAGCCTGACCCACAGGCCAACATCCTCATCCCAG
 GCACCCCTGGAGTCCGGCTGCCCTCAGAACATCTGACCTGCTGTGCCCTGGGCTGTGAGCAG
 GGGACACCCCCCTATGATCCTGGATAGGGACCTCCGTGTCCCCCCTGGACCCCTCCACAC
 CCGCTCCTCGGTGCTCACCCATCCACAGGCCAGGACCATGGCACCCAGCCTCACCTGTC
 AGGTGACCTCCCTGGGGCAGCGTGACCCAGAACAGACCGCCATCTAACGTGCTTAC
 CCGCCTCAGAACTTGACCATGACTGTCTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
 AAATGGCTCATCTCTGTCACTCCAGAGGGCCAGTCTCGCCTGGTCTGTGCAAGTTGATG
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCGACCCCTGTGCC
 TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCCTGGTGACCTGAGGGATGCAAGCTGA
 ATTACACCTGCAAGAGCTCAGAACCCCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
 AGAGCAAAGGCCACATCAGGAGTGACTCAGGGGGTGGTCGGGGGAGCTGGAGCCACAGCCCTG
 GTCTTCCCTGCTTCTGCCATCTCGTTGAGGTCTGCAAGGAAGAACATGGCAAG
 GCCAGCAGGGCGTGGGAGATACGGGATAGAGGATGCAAACGCTGCAAGGGTTGACCC
 CTCAGGGCCCTGACTGAACCTGGCAGAACAGACTCCAGGCTCAGCCCTCCAGGCC
 TCTGCCCTCCTCAGTGGGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
 GAAGCCTGGGACTCGCGGGACAGGAGGCCACTGACACCGAGTACTGGAGATCAAGATCC
 ACACATTGAGAAACTGCAGAGACTCACCCCTGATTGAGGGATCACGCCCTCCAGGCAAGGGA
 GAAGTCAGAGGCTGATTCTGTAGAATTACAGCCTCAACGTGATGAGCTATGATAACACT
 ATGAATTATGTGAGAGTGAAGACACAGGCTTAGAGTCAAAGTATCTCAAACCTGAAT
 CCACACTGTGCCCTCCCTTTATTTTTAACTAAAAGACAGACAAATTCCCTA

FIGURE 98

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCFSYPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLISRDAARRSDAGRYFFRMEKG
SIKWNYKHHRLSVNVTLTHRPNLIPIPGTLESGCPQNLTCSPWACEQGTPPMISWIGTSVS
PLDPSTTRSSVLTLPQPQDHGTSLTCQVTFPGASVTNKTVHLNVSYPPQNLTMTVFQGDG
TVSTVLGNSSSLPEGQSLRLVCADVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLNVSLQSKATSGVTQGVGGAGATALVFLSFCVIFVVVR
CRKKSSARPAAGVGDTGIEDANAVRGSAASQGPLTEPWAEDSPPDQPPPASARSSVGEGELOYA
SLSFQMVKPWDSRGQEATDEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 99

GACGCCAGTGACCTGCCGAGGTGGCAGCACAGAGCTCTGGAG**ATGA**AAGACCCTGTTCTG
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCTCACCTGGAGGAGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTCCGGAGGACAGGGAGGCCAGGA
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGCGGTGGGAAGTTGGAAGCCACGTTCACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGGAGGAAGCTCATGTAACCTGCAGGAGCTGCCAGGAGGACCACT
ACATCTTTACTGCAAAGACCAGCACCATGGGGCCTGCTCCACATGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTAAAGAAATTGGTGCAGCGCAAGGG
ACTCTCGGAGGAGGACATTTCACGCCCTGCAGACGGGAAGCTGCGTCCCAGAACAC**TAGG**
CAGCCCCCGGGCTGCACCTCCAGAGCCACCCCTACCACAGACACAGGCCGGACCACCT
GGACCTACCCCTCCAGCCATGACCCCTCCCTGCTCCCACCCACCTGACTCCAAATAAGTCCT
TTTCCCCCAAA

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FIGURE 100

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404
<subunit 1 of 1, 170 aa, 1 stop
<MW: 19457, pI: 9.10, NX(S/T): 0
MKTLFLGVTLGLAAALSFTLEEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHIFYCKDQHHGGLLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH
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Important features:

Signal peptide:

amino acids 1-17

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FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTCGGGACTGGAAGTCATCGGCAGAGGTCTCAC
 AGCAGCCAAGGAACCTGGGGCCCCTCCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA
 TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCCAGGATCATCAAGGGGTCGAG
 TGCAAGCCTCACTCCCAGCCCTGGCAGGAGCCCTGTTGAGAAGACCGGGCTACTCTGTGG
 GGCAGCAGCTCATGCCCGAGATGGCTCTGACAGCAGCCACTGCCTCAAGCCCCCTACA
 TAGTTCACCTGGGGCAGCACAAACCTCCAGAAGGGAGGGCTGTGAGCAGACCCGGACAGCC
 ACTGAGTCCTCCCCCACCCGGCTTCACAAACAGCCTCCAAACAAAGACCACCGAATGA
 CATCATGCTGGTGAAGATGGCATGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
 TCTCCTCACGCTGTGCACTGCTGGCACAGCTGCCTCATTCGGCTGGGCAGCACGTCC
 AGCCCCCAGTTACGCCCTGCCTCACACCTTGCAGTCGCCAACATCACCATCATTGACACCA
 GAAGTGTGAGAACGCCCTACCCGGCAACATCACAGACACCATGGTGTGCCCCAGCGTGCAGG
 AAAGGGGGCAAGGACTCCTGCCAGGGTGAETCCGGGGCCCTCTGGTCTGTAACCAGTCTCTT
 CAAGGCATTATCTCCTGGGGCAGGATCCGTGTGCGATCACCGAAAGCCTGGTGTCTACAC
 GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAA**TAG**ACTGGACCCA
 CCCACCACAGCCCATCACCTCCATTCCACTTGGTGTGGTCTGTCACTCTGTTAAC
 AAGAAACCTAAGCCAAGACCCCTACGAACATTCTTGGCCTCTGGACTACAGGAGATG
 CTGTCACTTAAATAATCAACCTGGGGTCGAAATCAGTGAGACCTGGATTCAAATTCTGCC
 GAAAATTGTGACTCTGGGAATGACAACACCTGGTTGTTCTGTTGATCCCCAGCCCCA
 AAGACAGCTCTGGCCATATATCAAGGTTCAATAAATATTGCTAAATGAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGGETRIIKGFECKPHSQWPQAALFEKTRLLCGATLIAPRWLLAAH
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSCLISGWGSTSSPQLRLPHTLRCANITIIIEHQCENAYPGNITDTM
VCASVQEGGKDSCQGDGGPLVCNQLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN
```

Important features:

Signal peptide:

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTCTGCTGGAGCCG**ATGCCAAAACCATGCATTCTTATT**CAGATTCAATTGTTT
TCTTTTATCTGTGGGGCCTTTACTGCTCAGAGACAAAAGAAAGAGGGAGAGCACCGAAGAA
GTGAAAATAGAACGTTTCCATCGTCCAGAAA**ACTGCTCTAAAGACAACCAAGAAGGGAGACCT**
ACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA
CACAAAATGAAGGCCACCCAAATGGTTGTTCTGGTGGCAAGTCATAAAGGCCTA
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCAGAAA**AGTAGTTATACCCCCCTTCATT**
TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACGGATGCTACATTGATTTTG
AGATTGAACTTTATGCTGTGACCAAGGACCACGGAGCATTGAGACATTAAACAAATAGAC
ATGGACAATGACAGGCAGCTCTCTAAAGCGAGATAAACCTCTACTTGCAAAGGGATTGAA
AAAAGATGAGAACGCCACCTGACAAGTCATATCAGGATGCAGTTAGAAGATATTTAAGA
AGAATGACCATGATGGTGTGGCTCATTTCTCCAAGGAATACAATGTATACCAACACGAT
GAACTA**TAGCATATTTGTATTTCTACTTTTTTTAGCTATTTACTGTACTTTATGTATA**
AAACAAAGTCACTTTCTCCAAGTTGCTATTTGCTATTTCCCTATGAGAAGATATTTGA
TCTCCCCAATACATTGATTTGGTATAAAATGTGAGGCTGTTTGCAAACCTTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 104

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDHDGDFISPKEYNVYQHDEL
```

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

FIGURE 105

CAGAAATGCAGGGACCATTGCTTCTTCAGGCCTCTGCTTCTGCTGAGCCTCTGGAGCT
GTGACTCGAAAACCAAAACTTCCGTGCTAAGTGCCCCCAAATGCTTCTGTGTCATAAA
CACTCACTGCACCTGCAACCATGGATATACTCTGGATCTGGCAGAAACTATTCACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGGCCCTGTAATCCAGTTCTTGGGAAG
CCAAGGCAGGGATCACCTGAGGTCAAGGAGTTGAGACCAGCCTGGCCAACATAGTGAAC
CCCAGTGTCTACTAAAAATACAAAAATCAGCCGGCGTGGTGGTGCATGCCATGCAATCCCAGT
TACTCGGGAGGCTGAGGCAGGAGAACCGCTGAACCTCAGGAGGCAGAAGTTGCAGTGAAACCC
AGATCCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGCTCTCAAAAGAAAAGA
TAGTTTCTTGTTCATTCGCGACTGCCCTCTCAGTGTTCCTGGATCCCCTCCAAATAA
AGTACTTATATTCTC

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FIGURE 106

MQGPILLPGLCFLLSLFGAVTQKTKTCAKCPPNASCVNNTHCTCNHGYTSGSGQKLFTFPL
ETCNARHGGSRL

Signal peptide:

amino acids 1-18

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FIGURE 107

CAAGCAGGTATCCCCCTGGTGACCTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGCAC
AGGGAAAGGGTGACCTCTGAGATTCCCCTTTCCCCAGACTTGGAAAGTGACCCAC**ATGG**
GGCTCAGCATCTTTGCTCTGTGTCTTGGCTCAGCCAGGCAGCCACACCGAAGATT
TTCAATGGCACTGAGTGTGGCGTAACTCACAGCCGTGGCAGGTGGGCTGTTGAGGGCAC
CAGCCTGCGCTGCCGGGGTGCCTTATTGACCACAGGTGGGCTCACAGCGCTACTGCA
GCGGCAGCAGGTACTGGTGCCTGGGAAACACAGCCTCAGCCAGCTCAGTGACCGAG
CAGATCCGGCACAGCGGCTCTCTGTGACCCATCCCGCTACCTGGAGCCTCGACGAGCCA
CGAGCACGACCTCCGGCTGCCTGCCCTGCCCTCCCGTAACCAGCAGCAGCTAAC
CCCTGCCCTGCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGC
ATCACCAACCACCCACGGAAACCCATTCCGGATCTGCTCCAGTGCCTAACCTCTCCATCGT
CTCCCATGCCACCTGCCATGGTGTATCCGGAGAACATCACGAGCAACATGGTGTGCAG
GCGGCCTCCGGGGCAGGATGCCCTGCCAGGGTGATTCTGGGGCCCTGGTGTGGGGGA
GTCCCTCAAGGTCTGGTGTCCCTGGGGCTGTGGGGCCCTGGACAAGATGGCATCCCTGG
AGTCTACACCTATATTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACA**TGAC**
CTGTTTCCCTCCACCTCCACCCCCACCCCTTAACCTGGGTACCCCTCTGCCCTCAGAGCAC
AATATCTCCCTCATCTTCCCTAGCTCCACTCTTGTGGCTGGAACTTCTGGAACTT
TAACCTCTGCCAGCCCTCTAAGACCCACGAGGGGTGAGAGAAGTGTGCAATACTCTGG
ATAAAATATAATGAAGGAGGGCAAAAAAAAAAAAAAA

FIGURE 108

MGLSIFLLCVLGLSQATPKIFNGTECGRNSQPWQVGLFEGTSIRCGVLIDHRWLTAAC
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRVTSSV
QPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVPQGDACQGDSGGPLVCGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

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FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCCTGTGCCTCCCTCGTCCCTCGC
 CGCGTCCCGAAGCCTGGAGCCGGCGGGAGCCCCGCGTCGCC**ATG**TGGCGAGCTCAGCA
 ACAGGTTCAAAGGAGGGAGGGCGTTCGGCTTGCTCAAAGCCGGCAGGGAGAGGAGGCTGGCC
 GAGATCAACCGGAGTTCTGTGTGACAGAAGTACAGTGTGAAGAGAACCTTCAGAAAA
 GCTCACAGCCTCAAAGAGAAAGTACATGGAGTTGACTGAACAATGAAGCGAGATTGACC
 TGATGTCTTAAGAGGATGATGGAGAACGTTGGTGTCCCAGACCCACTGGAGATGAAG
 AAAGATGATCTCAGAGGTGACAGGAGGGTCAGTGCACACTATATCCTACCGAGACTTGTGAA
 CATGATGCTGGGAAACGGTCGGCTGTCCCTCAAGTTAGTGTGATGTTGAAGGAAAGCCA
 ACGAGAGCAGCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCT**TGA**
 GGACCCCGCCTGGACTCCCCAGCCTTCCACCCCATACCTCCCTCCGATCTTGCTGCCCTT
 CTTGACACACTGTGATCTCTCTCTCATTTGTTGGTATTGAGGGTTGTTGTGTTT
 TCATCAATGTTGTAAGCACAATTATGCTCTTAAAGGGCTCTGGTCGGGAATCC
 TGAGCCTTGGTCCCCTCCCTCTTCTCCCTCCCTCCCGCTCCGTGCAAGAGGCTG
 ATATCAAACAAAAACTAGAGGGGCAGGGCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
 CTCACTTGGAGGAACCAGCACTCTCCATCCTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
 ACTGACACTGGCTCTGACGAGGACCCCAGGCCACTCTGAGAAGACCTGGAGTAGGGACAAGG
 CTGAGGGCCTCTTCGGTTCTGGACAGTGCCTGGTCCAGTGCTCTGGTCACCC
 AGGACACAGCCACTCGGGCCCGCTGCCCCAGCTGATCCCCACTCATCCACACCTCTTCT
 CATCCTCAGTGTGAGGTGGAAAGGAAAGGAGCTGGCATGGAGCCCTTCAAGAAGG
 TACCAAGGAACCTCCAGTCTGCTCTGGCCACACCTGTCAGGCAGCTGAGGGCAG
 CGTGCAGCCCTACTGTCCCTACTGGGGCAGCAGAGGGCTTGGAGGCAGAAGTGAGGCCTG
 GGGTTGGGGAAAGGTCAAGCTCAGTGTGTTCCACCTTTAGGGAGGATACTGAGGGGAC
 CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
 CTGAGAAATACAAGGTTGCTTGACCCAACTGCTTGAaaaaaaaaaaaaaaa

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMMLGKRSAVLKVM
MFEGKANESSPKPVGPPPERRDIASLP

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FIGURE 111A

CGCGCTCCCCGCGCCTCCGGGCTCACCGGTCTGGCCCGAGAGGCAGCCTCCCTCCA
 GGAGCGGGGCCCTGCACACCATGCCCCCGGGTGGGCAGGGTGGCCGCCCTGGCGCC
 CGCCCTGGCGCTGGCCCTGGCGCTGGCAGCGTCTGAAGTGGGCCTCAGCCGTGCCCTGCC
 CACCAAGTGTACCTGTCGGCTGCGAGCGTGCAGACTGCCACGGGCTGGGCCTCCGCCGCC
 CTCGGGGCATCCCCCGAACGCTGAGCGCTTGACCTGGACAGAAATAATATCACCAAGGATC
 ACCAAGATGGACTTCGGCTTGACAGAACCTCCAGTGAGCTTGCACTTGGAAAGACAACCAGGT
 CAGCGTCACTGGAGAGAGGCCCTTCAGGAGCTGAAGCAGTAGAGGACTGCGCTGAACA
 AGAATAAGCTGAAGTCTCCAGAATTGCTTTCCAGAGCACGCCAGCTCACCAACTA
 GATTGAGTAAAACCGATCCAGGGGATCCCGAGGAAGGGCTTCCGGGATCACCGATG
 GAAGAACCTGCAACTGGAACACACCACATCAGTGCAATTGAGATGGAGCCTCCGGAGCG
 TCGCGATTGGAGATCCTACCTCAACAAACAAACATCAGTCCTACATCTGGTCACAC
 TTCAACCACATGCCGAAGATCCGAACTCTGCCCTCAGTCAACCAACCTCTACTGGACTG
 CCACCTGGCTGGCTCTCGGATTTGGCTGGACAGCGAGCCAGTTGGCCAGTCAACTCT
 GCATGGCTCTTGCAATTGGGGCTTCACCTGGCGGATGTGCAAGAAGGAGTACGTG
 TGCCCAGCCCCACTGGAGCCCCATCTGAATGCCAACTCCATCTGCCCTTCGCC
 CTGCACGTGCAAGTAACATCTGGACTGTGAGGAAAGGGCTTGTGGAGATTCTGCCA
 ACTTGCGGGAGGGCATCGTCAAATAACCTGGCTAGAACAGAACACTCATCAAAGGCCATCTGCCA
 GGAGCCTTCACCCAGTACAAGAACATCGAACAGCATCAGCAAGGGCTCTGCCAGT
 TATTGCTCCAGATGCCCTCAGGGCTGAATCACTCACATCGCTGGCTCTGTATGGAAACA
 AGATCACCGGAGATGCGAACAGGGACTGTGTGATGGCTGGCTCTACAGCTGCTCTCC
 ATGCAACAAAGATCAACTGGCTCGGGTGAACAGCTTCAAGGACCTGAGAACCTCAACTT
 GCTCTCCCTGTATGACAACAAGCTGCAAGACCATCAGCAAGGGCTCTGCCCTCTGCAGT
 CCATCCAGACACTCCACTTAGCCAAAACCCATTGTGTCGACTGCCACTTGAAGTGGCTG
 CGCAGACTACCTCCAGGACACACATCGAGACAAGCGGGGCCGCTGCAGCAGCCGCCG
 ACTCGCAACAGCGCATCGCCAGATCAAGAGCAAGAAGTTCGGCTCTCAGGCTCCGAGG
 ATTACCGCAGGGTTCAAGCAGCGAGTGTCTCATGGACCTCGTGTGCCCGAGAAGTGTGCG
 TGTGAGGGCAGCATGTGGACTGTCCACAGGACAGTGGTCCGCATCCCCAACCCACTTCC
 TGAATATGTCACCGACTGCGACTGAATGAAATGAGGTATCTGTTCTGGAGGCCACTGGCA
 TCTTCAAGAAGTTGCCAACCTGGGAAAATAAAATCTGAGTAACAATAAGATCAAGGAGGTG
 CGAGAGGGAGCTTGTGAGGAGCAGCCGCTGAGGACTGATGTCGACAGGGAACCGACT
 GGAGACCGTGCACGGGGCGCTGTCTGGCTCAGTGGCTCAAACCTTGTGCTGAGGAG
 GTAACCTGATCAGCTGTGAGTAATGACACCTTGGCCGCTGAGTTCGGTGAGACTGCTG
 TCCCTCTATGACAATCGGATCACCAACATCACCCCTGGGGCTTACCCACGCTTGTCTCC
 GTCCACCATAAACCTCTGCCAACCCCTCAACTGCAACTGCCACCTGGCTGGCTCGGCA
 AGTGGTTGAGGAAGGGCGAGCTGCTAGTGGGAACCTCAGGTGCCAGAAGCCATTTC
 AAGGAGATTCCCATCCAGGATGTGGCATCCAGGACTTCACCTGTGATGGCAACGAGGAG
 TAGCTGCCAGCTGAGCCCGCGCTGCCCGAGCAGTGCACCTGTGAGGAGACACTGGTGCAT
 GCAGCAACAAAGGGGCTCGGCCCTCCCCAGAGGAGCATGCCAAGGATGTGACCGAGCTG
 CTGGAAAGGAAACCACTAACAGCGTGGCCAGAGAGCTGTCGCCCTCCGACACCTGACGCT
 TATTGACCTGAGCAACACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC
 ACCTCTCCACTCTGATCTGAGCTAACACGGCTGAGGTGCATCCCCGTCACGCCCTCAAC
 GGGCTGCCCTCGGAGCTAACCTCATGGCAATGACATTCCAGCGTCTCTGAAGG
 CTCCCTCAACGGACACTCACATCTCTTCCCATCTGGCGTGGGAACCAACCACTCCACTGTG
 ACTGCACTTGTGGTGGCTGTGGAGTGGTGAAGGGGGGTACAAGGAGGCCATCGCC
 CGCTGCAGTAGCCCTGAGCCCATGCTGACAGGCTCTGTCACCAACCCCAACCCACCGCTT
 CCAGTGCAGAACGGCCAGTGGACATCAACATTGTGGCAAATGCAATGCCCTCCAGCC
 CGTGAAGATAACGGACATGCACCCAGGACCCCTGTGGAGCTGTACCGCTGTGCCCTCCCC

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCACACACTGCATCCAGAACCCCTGTCA
 GCATGGAGGCCACCTGCCACACTGAGTGACAGGCCAACAGGATGGGTCAGCTGCTCTGCCCTC
 TGGGCTTTGAGGGGCGAGGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA
 AACAAATGCCACCTGCGTGAGGGATCAACAACATACGTGTATCTGCCGCTAACTACAC
 AGGTGAGCTATGCGACGGGGTATTGACCCTGTGTGCCCTGAGCTGAACCTCTGTACAGCATG
 AGGCCAAGTGCATCCCCCTGGACAAAGGATTCACTGCGAGTGTGCCCCACTACAGCGGG
 AAAGCTCTGTGAGACAGAACATGATGACTGTGTGCCCAACAGTGGCCACGGGGCAGGTG
 CGTGGACACAATCAATGGCTACACATGACCTGCCCAAGGGCTTCAGTGGACCCCTGTG
 AACACCCCCCACCACATGGTCTACTGCAAGGCCATGGACCAAGTACGAGTGGCAGAAC
 GGGGGCCAGTCATCGTGGTCAGCAGGAGGCCAACCTGCCGCTGCCACCCAGGCTTGGCCGG
 CCCCCAGATGGAGAAGCTCATCTGCAACTCTGTGGCAAAGACTCTACGTGAACTGG
 CCTCTGCCAAGGTCCGACCCAGGCCAACATCTCCCTGAGGTGGCCACTGACAAGGACAAC
 GGCATCTCTCTACAAAGGAGAACATGACCCCTGGCACTGGAGCTGTACCGAGGCCACGT
 GCGCTGGTCTATGACAGCTTGAGTCCCCCTCAACACACTGTACAGTGTGGAGACAGTGA
 ATGATGGGCAGTTTACAGTGTGGAGCTGGTACGCTAAACCAGACCCCTGAACCTAGTAGTG
 GACAAAGGAAGACTCCAAGGGCCTGGGAAGCTCAGGACAGCAGGAGCTAACAG
 CCCCTCTACCTGGAGGCATCCCCACCTCCACGGCTCTCGCCCTTGCGCCAGGGCACGG
 ACCGGCCTCTAGGCCTTCACGGATGCATCCATGAGGTGCGCATACAAACGAGCTGCA
 GACTTCAAGGCCCTCCACACAGTCCCTGGGGTGTACCAAGGCTGCAAGTCTGCCACCGT
 GTGCAAGCACGGCCTGTGCCCTGGAGAACAGGACAGGCTGGTGTGCGAGTGCCAG
 GCTGGACCGGCCACTCTGCCACGGGCCGGGAGGGGGCTGCCCTGCCACAGATGCCAC
 CATGGAAAATGTGTGGCACTGGGACCTCATACATGTGCAAGTGTGCCAGGGCTATGGAGG
 GGACTTGTGTGACAACAAGGAATGACTCTGCCAATGCCCTCAGCCTTAAGTGTCAACATG
 GGCAGTGCCACATCTGCCACAGGAGGGGGCCCTACTGCCCTGCCCAGGCCGGCTTACGGC
 GAGCACTGCCAACAAAGAGAACATCCGTGCCCTGGGACAAGTAGTGTCCAGGGTGTACGCC
 GAAAGGTTATGCTCATGTGCCACAGCCCTCAAGGTGCCCATCATGGAATGTGCGGGGCT
 GTGGGGCCCGAGTGTGCCAGGCCAACCCGCCAGCAAGCGGCCGGAAATACGTCCTCCAGTGCACG
 GACGGCTCTCTCTGGTAGAGAGGGTGGAGAGACACTTAGACTGTGCCCTGCCCTGGTTC
 C**TAA**GCCCCCTGCCGCCCTGCCCTGCCACCTCTGCCACTCCAGCTTGATGGAGTTGGACAGCC
 ATGTGGGACCCCTGGTATTGCACTGAGGAAATGAAGCTGGAGAGGAAGGTAAGAAGA
 AGAGAACATTTAGTATTTGTAaaaaataaaaaaaaatAGAACACTTTaaaaaaaaaaaaaaa
 AAAAAA

FIGURE 112

MAPGWAGVGAARVLALALASVLSGPPAVACPTKCTCSAASVDCHGLRAVPRGIPRN
 AERLDDLDRNNITRITKMDFAGLKNLRVLHLEDNQSVIERGAFQDLKQLERLRLNKNKLQVL
 PELLFQSTPKLTRLDSLENQIQQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL
 TLNNNNNISRLVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLQRRTVGQFTLCMAPVHL
 RGFNVADVQKKEYVCAPAPHSEPPSCNANSICSPSPCTCSNNIVDCRGKGLMEIPANLPPEGIV
 EIRLEQNSIKAIPIAGAFTQYKKLKRIKDISKNQISDIAPDADFQGLKSILSLLVLYGNKITEIAK
 GLFDGLVSLQLLLLNNANKINCLRVNTFQDLQNLNLLSLYDNKLQTISKGLFAPLQSIIQTLHL
 AQNPVFVCDCHLKWLDYLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSSEDYRSRFS
 SECFCMDLVCEPEKCRCEGTIVDCSNQKLVRIPLSHLPEYVTDLRLNDNEVSVLEATGIFKKLPN
 LRKINLSSNNKIKEVREGAFDGAASVQEMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV
 SNNTFAGLSSVRLLSLYDNRITTIPGAFTTLVSLSTINLLSNPNCNCNHLAWLGKWLKR
 RRRR
 IVSGNPRCQKPFKLKEIPIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRCNSNKGLR
 ALPRGMPKDVTELYLEGHNLTAVPRELSALRHLLIDLSNNNSIMLTNYTFSNMSSHLLTLL
 SYNRLRCIPVHFNGLRLSRVLTGHNDISSVPEGSFNDLTSLSHLALGTNPLHCDCSR
 RLW
 SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHRFQCKGPVDINIVAKCNACLSSPKNNGT
 CTQDPVELYRACPYSYKGKDCTVPINTCIQNPCQHGHTCHLSDSHKDGFSCSCPLFEGQR
 CEINPDDCEDNDCCENNATCVDGINNYVICCPPNYTGELCDEVIDHCPPELNLCQHEAKCIP
 PL
 DKGFSCECVPGYSGKLCETDNDDCAVHKCRHGAQCVDTINGYTCTCPQGFSGPFCEHPPPMV
 LLQQTSPCDQYECQNGAQCIVVQQEPTCRCPGFGAPRCEKLI
 TIVNFVGKDSYVELASAKVRP
 QANISLQVATDKDNGILLYKGNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDQFHS
 VELVTLNQTLNLVVDKGTPKSLGKIQKQPAVGINSPLYGGIPTSTGLSALRQGTDRPLGGF
 HGC
 IHEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVVCECRPGWTGPLC
 DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKNDSANACSAFKCHHQCHISD
 QGEPYCLCQPGFSGEHCQQENPCLGQVREVI
 RRQKGYASCATASKVPI
 MECRGCCGPQCCQ
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLAC
 S

Signal peptide:

amino acids 1-27

FIGURE 113

GGATGCAGGACGCTCCCTGAGCTGCCTGTCAACGACTAGGTGGAGCAGTGTTCCTCCGCA
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAAGGAATCTGCCTTTCAGTTCTGTCT
CCGGCAGGCTTGAGG**ATG**AAGGCTGGGGCATTCTGACCCCATGGCTGCCTGGTCACAG
GCGCCGAGTCAAATCTACACTCGTTGCAAACGGCAAAATATTCTCGAGGGCTGGCCTG
GACAATTACTGGGCTTCAGCCTTGGAAACTGGATCTGCATGGCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGTCTGGATGACGGCAGCATCGACTATGGCATCTTCAGATCA
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGGAAACAACCACTGCCATGTCGCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAATTGTTAAAGA
GACACAAGGAATGAACATTGGCAAGGCTGGAAGAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGAAAAAAAGGCTGTGAGGTTTCC**TAA**ACTGGAACCTGGACCCAGGATGCTTGAGCAAC
GCCCTAGGATTGCACTGAATGTCCAATGCCGTGTCATCTGTCCCCTTCCCAATA
TTCCCTCTCAAACATTGGAGAGGGAAAATTAGCTATACTTTAAGAAAATAATTTCCAT
TTAAATGTC

FIGURE 114

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCVA
CSALITDDLTAIIICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

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FIGURE 115

CAGGCCATTGCATCCCACTGTCCTGTGTTGGAGGCCAGGCCACACCGTCCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATCATGCCCCATTAAAACTTGTACATGGCTCCC
 CATTGGTTTGGAGAAAAGTCAAGCTTTACCTTGGTGTCTGCCTGTATCCAGTGTTC
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTACTGTCACTTCCAGATCTGCTCTCAC
 CAAGAGAGATTCTTTCTAACGACTATACAGGGCCCAATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTTAAGTCAACAGCCAGTTCACAGCTGTTTAAGGAA
 ACATTCAAGTCCCTGTCTCACATAGACCCGTATGTCCTCTATCCATCTAAATGTACCAG
 CTTTGACTCAGTGTCTGAAAGCTGGATGACCTAGTCCCCAAGGGAAAAATTCTGC
 TGCTCTCCATCAACAGATAAGGAAAGAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
 CAGCTGCGTGGAGATTGACATCCCAAGATTGGGAGGGTTCATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGCCAAC
 AGTCCGACCTTGGCCAGTATGTGACCTTCTGAGGCTTTCTCAGACAAACAGAAAATCTCC
 CTCTCCACAGCTGCACGTGTGCTTACACACCAAGCAATGAGCAGTGGCATTGTCCC
 TCTGGAAGCCATGTACATGCAGTGCCAGTCATTGCTTAAATTGGTGGACCCCTGGAGT
 CCATTGACCACAGTGTACAGGGTTCTGTGAGGCTGACCCGGTGCACCTCTCAGAAGCA
 ATAGAAAAGTCATCCGTGAACCTCCTAAAGGCCACCATGGGCCTGGCTGGAAGAGGCCAG
 AGTGAAGGAAAATTTCCTGAAAGCATTTACAGAACAGCTTACCGATATGTTACCAAAC
 TGCTGGTATAATCAAGATTGTTTAAGATCTCCATTAAATGTCATTGATGGATTGAGACC
 CAGTTTGAACCAAAAAGAAACCTAGAATCTAAATGCAAGAGATCTTTAAAAAATAAA
 CTTGAGTCTGAATGTGAGCCACTTCTTATACACACACCTCCGTCCACTTTCAAGAAA
 AACCATGTCCTTATGCTATAATCATTCCAAATTGGCAGTGTAAAGTTACAAATGTTGGT
 TCATTCCATGTCAGCAGAGTATTAAATTATTTCTGGGATTATTGCTCTCTGTCTA
 TAAATTGAAATGATACTGTGCTTAATTGGTTTCATAGTTAAGTGTATCATTCAA
 AGTTGATTAATTGGCTCATAGTATAATGAGAGCAGGGTATTGTAGTCCAGATTCAA
 CCACCGAAGTGTCACTGTCATCTGTTAGGGATTGGTTGCTCTGTCTTGCTGGATC
 CATAGCGAGAGTGTCTGTATTGTTAAGATAATTGTATTGCAACTGAGATATAA
 TAAAAGGTGTTATCAAAAAAAAAAAAAAA

FIGURE 116

MPLLKLVHGSPLVFGEKFKLF TLVSACIPVFRILARRKKILFYCHFPDLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTA AVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
DLVPKGKKFLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHILIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTFLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPD PVHFSEAIEKFI REPSLKATMGLAGRARVKEKF SPEAF
TEQLYRYVTKL V

Signal peptide:

amino acids 1-15

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FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGCGGCAGAACCAATGTTGGACTTCGCGATCTT
 CGCGCTTACCTTCTGCTGGCCTGGGGAGCCGTGCTACCTCTATCCGGCTCCAGAC
 AAGCTGCAGGAATTCCAGGGATTACTCCAACTGAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGGAAAGTTGCATGAGTTCTGGTTAATTGCATGAGAGATATGGGCTGTGGT
 CTCCCTCTGGTTGGCAGGCCTCGTGGTAGTTGGGACTGTTGATGACTGAAGCAGC
 ATATCAATCCAATAAGACATCGGACCCCTTTGAACCATGCTGAAGTCATTAAAGGTAT
 CAATCTGGTGGCAGTGTGAGTGAACCAACATGAGGAAAAAATTGTATGAAATGGTGT
 GACTGATTCTCTGAAGAGTAACTTGCCCTCCTCAAAGCTTCAAGAAGAATTATTAGATA
 AATGGCTCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTGGTTTGCT
 ATGAAGTCTGTTACACAGATGTAATGGTAGTACATTGAAGATGATCAGGAAGTCATTG
 CTTCCAGAAGAACATGGCACAGTTGGCTGAGATTGAAAAGGCTTCTAGATGGTCAC
 TTGATAAAAACATGACTGGAAAAAACAAATATGAAGATGCCCTCATGCAACTGGAGTCGT
 TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTCAGTCACATATTTCTGT
 CTTAGTACAAGGGAACCTTAATGACCACAGATCCTAGAACAGACTATGATATTCTCTGG
 CCAGTTGCATAATAACTGCAAATTGTGTACCTGGCAATCTGTTTTAACCACTCTGAA
 GAAGTCAAAAAAAATTATATGAAGAGATAAACCAAGTTGGAAATGGTCTGTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGCTTGTGAAACTGTCGAACGCCA
 AACTGACTCCAGTTCTGCCAGCTCAAGATATTGAAGGAAAATTGACCGATTATTATT
 CCTAGAGAGACCTCGTCCTTATGCCCTGGTGTGGTACTTCAGGATCCTAAACTTGGCC
 ATCTCCACACAAGTTGATCCAGATCGTTGATGATGAATTAGTAATGAAAACCTTCC
 CACTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTGCATATATGGTACCC
 GTACTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTCTGTGGAGGGACAGGTTATTGA
 AACAAAGTATGAACTGGTAACATCATCAAGGGAGAAGCTGGATCACTGTC
 AACAGAT
ATTTAAATTTATACATTAAATCATTAAATTGATTGAGGAAAACAACCATTAAAAAA
 AAATCTATGTTGAATCCTTTATAAACCAGTATCACTTGTAAATATAACACCTATTGTAC
 TTAA

FIGURE 118

MLDFAIFAVTFLLALVGAVLYLPPASRQAAGIPGITPTEEKDGNLPLDIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLVVSLGTVDVLKQHINPNKTSDFETMLKSLLRYQSGGGSVSENHMRK
KLYENGVTDSLKNFALLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMSGSTFE
DDQEVRFQKNHGTWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTTSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVLCETVRTAKLTPVSAQLQDIEGKIDRFIIIPRETLVLYALGVVL
QDPNTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQECPELRFAYMVTVLLSVLVKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 119

CTAGATTGTCGGCTTGCAGGGAGACTTCAGGAGTCGCTGTCTCTGAACCCAGCCTCAGA
GACCGCCGCCCTGTCCCCGAGGGCCTGGGCCGGGCTCTCAGGGCTGTGCCCTCTCGCTC
CTGACGCTCTGGCGCATCTGGTGGTCATCACCTTATTCTGGTCCCAGGACAGCAACAT
ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCACTGG
TGGCCGCGCTCTGTACCCCTGGGCTCTTGCACTGGAGCTGGCGTTCCCTCAGGA
GTCTCCATGTTAACAGCACCCAGAGCCTCATCTCCATTGGGCTCACTGTAGTGATCCGT
GGCCCTGTCTTCTTCATATTGAGCGTTGGAGTGCACTACGTATTGGTACATTTGTCT
TCTGCAGTGCCTTCCAGCTGTCACTGAAATGGTTTATTGTCACCGTCTTGGCTGAAA
AAGAAACCCCTCTGATTACCTTCATGACGGGAACCTAACGGACGAAGCCTACAGGGCAAGGG
CCGCTTCGTATTCTGGAAAGGAAGGCATAGGCTTCGGTTTCCCTCGAAACTGCTTC
TGCTGGAGGATATGTGTTGAAATAATTACGTCTGAGTCTGGATTATCCGCATTGTATT
GTGCTTGTAAATAAAATGTTGTAGTAACATTAAGACTTATACAGTTTAGGGGACA
ATTAaaaaaaaaaaaa

FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACIPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT
EMALFVTVFGLKKPFI

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

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FIGURE 121

TCCCCGACCCCTGCCGCCCTGCCACTATGTCCC GCC GCT CTATGCTGCTTGCCCTGGGCTCTCC
CCAGCCTCCTCGACTCGGAGCGGCTCAGGAGACAGAAAGACCCGCCCTGCTGCAGCCCCATA
GTGCCCGGAACGAGTGGAAAGGCCCTGGCATCAGAGTGCGCCAGCACCTGAGCCTGCCCTT
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCCTGTCAGC
AGCAGGCCCGAATGTGCAAGCACTACCACATGAAGACACTGGGCTGGTGCAGTGGCTAC
AACTTCCTGATTGGAGAACAGGGCTCGTATACGAGGGCCCTGGCTGAAACTTCACGGGTGC
CCACTCAGGTCACTTATGGAACCCCATGTCCATTGGCATCAGCTTCACTGGCAACTACATGG
ATCGGGGTGCCACACCCAGGCCATCGGGCAGCCCAGGGTCACTGGCCTGCGGTGTGGCT
CAGGGAGCCCTGAGGTCCAACATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCCTGAGGCC
CTGCTGATCCGACCCCATCCCTCCCTCCATGGCAAAAACCCCACTGTCTCCTCTCCA
ATAAAAGATGTAGCTC

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FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHISLPLRYVVVSHT
AGSSCNPASCQQQARNVQHYHMKTTLGCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPPTQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

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FIGURE 123

CTGGGACCCGAAAAGAGAAGGGGAGAGCGAGGGGACAGAGCGGAGGAAG**ATG**CAACT
 GACTCGCTGCTGCTCGTGTTCCTGGTGAGGGTAGCCTCATCTGGTCATCTGTGGCCAGG
 ATGATGGTCCTCCGGCTCAGAGGACCTGAGCGTGTGACCACAGGGGCCAGCCCCGGCC
 CGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAACGTCAGTCCGCCCATGGCAATTCCACTCT
 CCTAGGGCTGCTGGCCCGCCTGGGAGGCTTGGGCATTCTGGCAGCCCCCAACCGCC
 CGAACCCACAGCCCCCCCACCTCAGCCAAGGTGAAGAAATCTTGGCTGGGCACATTCTAC
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCACCAGGAACAGCAGATCTTCATCGAACGCCAAG
 GCCTCCAAATCTTCACTGCCGGATGGAGTGGAGAACGGCTGAGAACCGGGCCGCCGACCTC
 GCTTTGCACCCACGACCCAGCCAAGATCTGTCCTCGAGACACGCTCAGAGCTCAGCCACCT
 GGAGCTGCTCCAGCCCTCAAAGTCGTCGTGTCTACATCGCTTCTACAGCAGGACTAT
 CGGCTGGTCCAGAACGGTGTGCCAGATTACAACCTACCATAGTGTACCCCCCTACTACCCATC
 TGGG**TGA**CCCCGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAAGGACAGGCCCTGCCCATGC
 AGGAGACCATCTGGACACCGGGCAGGGAAAGGGGTTGGCCTCAGGCAGGGAGGGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGCCAGGGCAAGTCTCAAGTGGCAGAGAAAGGGTCCAAGTG
 CTGGTCCCACCTGAAGCTGTGGAGTGAAGATCACAGGAGCACTGGAGGAGGAGTGGCT
 CTCTGTGCAGCTCACAGGGCTTGCCACGGCACAGAGAGATGCTGGGTCCCCAGGGCC
 TGTGGCAGGCCATCAGTGTGGCCCAAGATCAAGTCATGGAGGAAGCTAACCTGGTT
 CTTGCCATCCTGAGGAAGATAGCAACAGGGAGGGGGAGATTTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCTTAGGAGGCCAGTCAGCAGGGTGGGTGGGC
 CAGAGGAGCTCCAGCCCTGCCTAGTGGGCCCTGAGCCCCCTGCTGTGCTGAGCATG
 GCATGAGGCTGAAGTGGCAACCCCTGGGTCTTGATGTCTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTCCAAAATCCCTTCTGCCAGTACTCCCCCTGTACCAACCCATT
 GCTGATGGCACACCCATCTTAAGCTAACAGACAGGAGATTGCTGGCTCCACACTAACAGGCC
 ACAAGCCCATCCCGTGTGTGTCCTTCCACCCCAACCCCTGCTGGCTCCCTGGGAG
 CATCCATGTCCGGAGAGGGGCTCCCTAACAGTCAGCCTCACCTGTCAGACCCGGGGTCTCC
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGGGGGGGGGCAGAGA
 GCATGTGCTGGATCTGTTCTGTGTCTGTGGTGGGGGGAGGGAGGGAAAGTCTTGT
 GAAACCGCTGATTGCTGACTTTGTGTGAAGAACATGTTCTGGAGCAGGAATAAGCTT
 GCCCCGGGGCA

FIGURE 124

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNCTFSVHFQHNATGQGNISISLVPSSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPKVVCVYIAFYSTDYRLVQKVCVDNYHSDTPY
YPSG
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Important features of the protein:**Signal peptide:**

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTGATGACTTCAAGATGTCAGAGACAGAGTGGGTGCAGGGCCCCA
 GGCAGGGCTGATTCTTGGCGGAGGAGAGTAGGGTAAAGGGTCTGCATGAGCTCCCTAAAG
 GACAAAGGTAACAGAGGCCAGCAGAGAGCTGAGGGGAGACTTGACTTCAGGCCACAGAAT
 TGGTGGAAAGTGTGCGCGCCGCCGCCGCGCTCGCTCCTGCAGCGCTGTCGACCTAGCGCTAG
 CATCTCCCAGCACCGGGATCCCGGGTAGGAGGCAGCGGGCGAGCACCGCCAGCC
 GGCTGCGGCTGCCACACGGCTCACC**AT**GGCTCCGGCGCCGGCGTGTCCGGCTGCCG
 GCCGTGCTGTTCTCACGCTGCCGGCTGCCGCTGGGACAGAACGACACGGAGCC
 CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGCCACGGACTCCAAGG
 GCTCCTCTTCTCCCGCTGGGATATCGTCGGGGCGCCAACCTCAAAGGTGCGCTTCTCG
 GCGGTGCGGAGCACCAACCAACAGAGCCATCGAGATGAGCAACAAGACGCCATTTACTT
 CGATCAGATCTGGTGAATGGGTAATTTCACATTGGAGTCTGCTTTGTACCAACAA
 GAAAAGGAATTACAGTTTCACTGGTCTGGGAGGCTGGCAGTATTCACGTTCTGGCTTCTGGT
 GTTAACATTGATTTAAATGGAAAACCAGTAATATCTGCCCTTGCGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGTCTGCTACTAGATAAAGAGGATAAGGTTACCTAA
 AACTGGAGAAAGTAATTGGTGGAGGCTGGCAGTATTCACGTTCTGGCTTCTGGT
 TTCCCCCTA**TAG**GATTCAATTCTCCATGATGTTCATCCAGGTGAGGGATGACCCACTCTG
 AGTTATTGGAAGATCATTTCATCATGGATTGATGTTCTGGTTCTCATGGGTG
 GATATGGATTCTAAGGATTCTAGCCTGCTGAACCAATACAAAATTTCACAGATTATTG
 TGTGTCGTTCACTGGATTGGACTCTAACGAGATAATACCTATGCTTAAATGTA
 ACAGTCAAAAGCTGCTGCAAGACTTATTCATGAAATTCTCATTCCTGGGTTACTGAATTAGT
 TACAGATGTTGAAATTATTGTTAGTTAAAGACTGGCAACCAAGGTCTAAGGATTAGA
 AAACCTAAAGTCTGACTCAATCAACGGTTAGTGTGATACTGCCAAAGAAACTGTATACTG
 TGTTAATATATTGATTATTGTTTATTCTCTGGAAATTAGTTGTTGTTCTGTAA
 AAAACTGGATTTTCTGACTAACGGTATTATGTTCTCTTAAATAAGGTAAATGAA
 TGCTTGGCCACAAATTACCTGACTACGATATCATCGACATGACTTCTCTAAAAAA
 GAATGCTTCATAGTTGTTAATTGATATGTAAGAGTCATATTTCACAGATTATATT
 TTCTAAGAAGAAGAATAGATCATAATCTGACAAGGAAAAGTTGCTTACCCAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCTCCGAGGGAAATCTTAACTTATTG
 TCAACTTTAAATTAAATGATTGATAATAACCACTTATTAAAAACCTAAGGTTTTTT
 TCCGTAGACATGACCACTTATTAACTGGTGGTGGGATGCTGTTCTAATTACCTAT
 TTTCAAGGCTCTGTTGATTGAAAGTATCATCTGGTTTGCTTAACTCTTAAATTGTA
 TATATTATGTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTAGTGC
 CATTGCTTTGATAGGTCAATGAAATTCAAAATTATTATGCTGTTATAGAATAAAGA
 TTAATATGTTAAAAAA

FIGURE 126

MGSRRRALSAVPAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSNPATDSKGSSSPLGI
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIYFDQILVNNGNFFTLESVFVAPRKGIYSFSF
HVIKVYQSQTIQVNMLNGKPVISAFAGDKDVTREAATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

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FIGURE 127

CGGTGGCC**ATG**ACTGCGGCCGTGTTCTCGGCTGCGCCCTCATGCCCTCGGCCTGCGCTC
GCCCTTATGTCCTCACCATGCCATGAGCCGTTGCGTATCATCTCCTCATGCCGGAGC
TTCTCTGGTTGGTGTCTACTGATTGCTCCCTGGTTGTTGATGGCAAGAGTCATTA
TTGACAACAAAGATGGACCAACACAGAAATCTGCTGATCTTGAGCGTTGCTCTGTC
TATATCCAAGAAATGTCGATTTGCATATTATAAACCTCTTAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAACCCAGGTGAGACAGCACCCCTATGCCACTGCTGCCCTATGTTCTGGCT
TGGGCTTGGAAATCATGAGTGGAGTATTCCTTGTGAAATACCCCTATCTGACTCCTGGGG
CCAGGCACAGTGGGCAATTCTGGAGATTCTCCTCAATTCTCCTTATTCAAGCTTCATGAC
GCTGGTCATTATCTGCTGCATGTATTCTGGGCATTGTATTTTGATGGCTGTGAGAAGA
AAAAGTGGGGCATCCTCTTATCGTCTCCCTGACCCACCTGCTGGTGTCAAGCCCCAGACCTTC
ATAAGTTCTATTATGGAATAAACCTGGCGTCAGCATTATAATCTGGTGCTCATGGGCAC
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCAAGCCTGAAACTCTGCCTGCTCTGCCAAG
ACAAGAACTTCTCTTACAACCAGCGCTCCAGA**TAA**CCTCAGGGAACAGCACTCCCAA
ACCGCAGACTACATCTTAGAGGAAGCACAACGTGCTTTCTGAAAATCCCTTTCTG
GTGGAATTGAGAAAGAAATAAAACTATGCAGATA

FIGURE 128

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLGP GTVGIGHGDSPQFFLYSAFM TLVIILLHVFWGIVFFDGCEKKW
GILLIVLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGCRSLKLCLLCQDKN
FLLYNQRSR
```

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

FIGURE 130

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLGPKNVSKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVVRQKEAVVSVFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNNTYQLRVRSMRDFVLRLTGEQFSFNTAAQPYFKYEFPEGVDSVI
VKVTSNKAFPPCSVISIQDVLCPVYDLDDNNVAFIGMYQTMTKKAATVQRKDFPSNSFYVVVV
VKTEDQACGGSPLPFYYPFAEDEPVQDQGHROKTLVLSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKTLLVAIDRACPESGHPRVLADSFPGSSPYEGYNNGSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEPVGTRPRVDSMSSVEEDDYDTLDIDSDKNVIRTKQYLYVADL
ARKDKRVLRKKYQIYFWNIATIAVFYALPVVQLVITYQTVNNVTGNQDICYYNFLCAHPLGN
LSAFNNILSNLIGYILLGLLFLIIILQREINHNRAALLRNNDLCALECGIPKHFGLFYAMGTALM
MEGLLSACYHVCNPNTNFQFDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTAFWIVFSIIHIIATLLLSTQLYYMGWRWKLDGIFRRILHVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLICIVCTS VVWGFA LFFF QGLSTWQKTPAESREHNRCDCILLDFFDDHDWIWFLLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF
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Important features of the protein:

Signal peptide:

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTCCCCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTCTTGTGCTGGCAGCTGGACCAAGGGAGGCCAGTCCTGGCGCTGGAGGGCTGTCTG
ACCATGGTCCCTGCCTGGCTGTGCTTGTCTGGCTCCCTCCCCAGGCTCTCCAAGGC
 CCAGGCTGCAGAGCTGTGTGAAGTTCAGAAAATCTGGAAATTCTCCCTTATAC
 TGACCAAGTGTGCCGTGCCCCCTGAGGGGGCTGAAGGGCAGATCTGCTGTCAAGGGACTCA
 GGCAAGGCAACTGAGGGGCCATTGTCTATGGATCCAGATCTGGCTTCCGTGGCTGG
 GGCCTGGACCGAGAGGAGCACGGCAGAGTACAGGTACAGGTACCCCTGGAGATGCAGGATG
 GACATGTCTTGTGGGGTCCACAGCTGTGCTTGTGACGTGAAGGATGAGAATGACCA
 CCCCTTTCTCAAGCCATCTACAGAGCTGGCTGGCTGGCCGGGTACCCAGGGCTGGCATCCC
 CTTCCTCTTCTTGTGGCTTCAGAGGGGATGAGGCAAGCAGCCAACCTGGATCTTCGAT
 TCCACATCTTGAGCCAGGCTTCAGCCCCAGCCTTCCCGACATGTTCAGCTGGAGGCTCG
 CTGGGGCTCTGGCCCTCAGCCCCAAGGGAGCACCCGCTTGACCCAGGCCCTGGAGGAG
 CTACACGCTGTGCTACAGGTCAAGGACATGGGTGACCCAGGCCCTGGAGGCA
 CCACCGTGGAAAGTCTCATACAGAGCACCTGGTGTCTCTAGACCTATCCAC
 GAGAACATCTCAAAGTCTTACCCGACACATGGCCAGGTACACTGGAGTGGGGTGATGT
 GCACTATCACCTGGAGAGGCATCCCCGGGACCTTGTGAAGTGAATGCAGAGGAAACCT
 ACGTGGACCAAGAGAGCTGGACAGAGAACCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
 ATTCCCATGGCGAGGACTATGGCCCTCTGGAGCTCACGTGCTGGTGTAGGATGAGAA
 TGACAACGTGCTTATCTGCCCTCCCGTGAACCCACACTCAGCATCCTGAGCTCAGTCCAC
 CAGGTACTGAAGTGAAGTCTGAGCAGAGGATGAGCATGGCCCTGGCTCCCCAATTCT
 CACGGTGTATCAGCTCTGGCCCTGGAGCTGTGAGGATGGGGTAGAGGGGAGACCTTCCA
 GGTGGACCCCACCTCAGGCACTGTGACGCTGGGGGTGCTCCACTCCAGCAGGCCAGAAC
 TCTGCTTCTGGTGTGGCATGGCAGGACCTGCAGGCGCAAGGGTGGCTTCAGCAGCAGTGT
 AAAGCTGGAAGTGCAGTCAGATATCACTGACAGGCTCTGGTGTGGCATCTCCAGAT
 TGGCCCTATAAGCTCTTGTGGAGATGTGGAGCCGGACTCTGGTGGCATGTAACAGCCA
 TTGATGCTGACCTCGAGCCGCCCTCCGCCTCATGGATTITGGCATTGAGAGGGAGACACA
 GAAGGGACTCTGGCTGGATTGGAGCACAGACTCTGGCATGTTAGACTCAGACTCTGCAA
 GAACCTCACTTATGAGCGAGCTTCAAGTCAGGATGGTGTGGTGTGGCAGACTGTGGGA
 AGCTGGTGGGGCAGGCCAGGCCCTGGAGGCCACGGCACGGTGACTGTGCTAGTGGAGAGA
 GTGATGCCACCCCAAGTGGACCCAGGAGAGTACAGGCCAGTGTCCCAACTGTGCC
 AACGGGCTTCTCTGTGACCATTCAGGCCCTGGCACGGGACTCTGGTGGCATGTA
 CCCTAGTCATGACTCAGAGGGCTGCTCTGCATTGAGAAATTCTCCGGGAGGTGCACACC
 GCCCAGTCCCTGCAGGGCCGCCAGCTGGGACACCTACAGGTGCTTGTGGAGGCCAGGA
 TACAGGCCCTGACTCTGGCCCTGTGCCCTCCAAATACCTCTGCACACCCCGCCAAGACCATG
 GCTTGATGCTGGTGTGGACCCAGAAGGACCCGATCTGGGACAGCTGGTGTCTTAC
 TTCACCCCTGGTCCCAACCCACGGTCAACGGGATTGGCCCTCCAGACTCTCAATGGTT
 CCATGCCCTACCTCAGGCCCTGCATGGGTGGAGGCCAGGTGAACACATAATCCCCGTGG
 TGGTCAGGCCAAATGCCAGATGTGGCAGCTCTGGTGTGGTGTGGAGGCTGGCAAC
 GTGGAGGGCAGTGCATGCCAGGGCATGAAGGGCATGCCACAGAAGCTGTGCC
 ACTGGGCATCTTGTAGGCACCCCTGTAGCAATAGGAATCTCCCTCATCTCTCA
 ACTGGGACCATGCAAGGAAGAAGGACCCGATCACAGGAGCACAGAGCTGCCCTGAAGGG
 ACTGTCTGAATGGCCAGGCCAGCTCTAGCTGGAGCTTGGCTCTGGTCCATGTAGTCCC
 CTGGGAGAGAGGCCAGCACCAAGATCCAGCAGGGACAGGACAGAGTAGAAGCCCTCCAT
 CTGCCCTGGGGTGGAGGCCATCACCATCACAGGACATGTCTGCAGAGCCTGGACACCAAC
 TTATGGACTGCCATGGAGTGTCCAAATGTCAGGGTGTGGCCAAATAAAAGCCCCA
 GAGAACTGGCTGGCCCTATGGGAAAAAAAAAAAAAAAG

FIGURE 132

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSDGSG
 KATEGPFPAMDPSGFLLVTRALDREEQAQEYQLQVTLEMQDGHLWGPQPVLVHKDENDQVP
 HFSQAIYRARLRLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRL
 GALALSPKGSTS LDHALERTYQLLVQVKDMGDQASGHQATATVEVSIIESTWVSLEPIHLAE
 NLKVLYPHHMAQVHWSGGDVHYHLESHPGPFEVNAEGNLYVTRELDRREAQAELYLLQVRAQN
 SHGEDYYAAPLELHVLMDENDNVPICPDPRTVSIPELSPPGTEVTRLSAEDADAPGSPNSH
 VVYQLLSPEPEDGVGRAFQVDPTSGSVTLGVPLRAGQNILLVLAMDLAGAEGGFSSTCE
 VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMITAIDADLEPAFRLMDFAIERGDTE
 GTFGLDWEPDSGHVRRLCKNLSEYAAPSHEVVVVVQSVAKLVGPGPGPATATVTVLVERV
 MPPPKLDQESYEASVPISAPAGSFLLTIQPSDPISRTLRFSLVNDSEGWLCLIEKFSGEVHTA
 QSLQGAQPGDTYTTLVEAQDTALTLPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
 TLGPNTVQRDWLQTLNGSHAYLTALHWVPREHIIPVVVSHNAQMQLLVRVIVCRCNV
 EGQCMRKVGRMKMPTKLSAVGILVGTVAIGIFLILITHWTMSRKKDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGAC**ATG**AGGGTGGACTGTTCATTGGGCCCTATTGGGTCCAGCATCTGTGGCAA
 GAAAAAATTTTGGGGACCAAGTTGGGATTAATGTCAAGGCTAACTTCTGAAATCTCCCTCCT
 ATTGAGTCAACTAGTGAATTCAAACAATTGAGCTCAATTCTGGAATCTCCCTCCT
 TCAATCGGCCGTGGATCTCTGGCCATCTGAGCTGCAGGATTTAACCTCCCT
 AGATCCCAGGGCTTAGAGTACGAGTGAACATTGAGGACCTGCAGGCCCTTTAGACAATGA
 AGATGATGAAATGCAACACAATGAAGGCCAGAACCGAGCAGTAATAACTTCAACTACGGGG
 CTTACCATCCCTGGAAAGCTATTACACCGAGATGGACAAACATTGCCAGACTTCTGAC
 CTGGCAGGGGGTGAAGATTGGACATTGTTGAAACCGGCCGATGTATGACTGAAGTT
 CAGCACTGGGAAAGGCGTGAGGCCGGCGCCCTTGGCTGAATGCAGGCCATCCTCCAGAG
 AGTGGATCTCCAGGCCACTGCAATCTGGACGCCAGGAAGATTGTATCTGATTACAGAG
 GATCCAGCTATCACCTCCATCTGGAGAAAATGGATATTCTCTGCTGCTGCCAATCC
 TGATGGATATGTATACCAAACCGATTATGGAGGAAGACGCCGGTCCGAAATC
 CTGGAGCTCTGGCATTTGGCTGACCCAAATGAGAAACTGGAAACGCTAGTTTGAGGAAAG
 GGAGCCAGGCCAACCCCTGCTCCAGACTGACCCACGCCAATTGGAAGTGG
 GCTGAAATCAGTGGTAGATTTCATCAAAAATGGGATTTCAGGGCTTCATGACCTGC
 ACAGCTACTCCAGCTGCTGATGATTCATGGTACTAGTCAGTCAGTCAGTCAGTCAG
 GAGGAAGTCGACAAGGTGGCGAGGCTTGGGCCAAAGCTGGCTTCCTGTCGGCACTGA
 GTACCAAGTGGCTCCACCTGGCACCAGCTGCTATCCAGCTAGCGGGACAGCATGACTGG
 CGTATGACAACGGCATCAAATTGCAATTGAGTTGAGAGATACCGGGACCTATGGC
 TTCTCTGGCAGCTAACAGATGCTGGCCACTGCAAGGAGACGCTGGCTGGGCTGAAGAC
 CATCATGGAGCATGTCGGGACAACCTCTAC**TAGGCGATGGCTCTGCTCTGCTAC**
 TTGTCACCCACAGTCGACCCACTGAGGCCATTGTTAAAGGAGCTTTCTACCTGTGAG
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCTGCCCTCTCCAGCCAGCTCCCTGGAGT
 CGTGTGTCCTGGCTGGCTGGCAAGAACACTGGTCTGCCAGCCTGCTCAATTGCTCTG
 CTGTTTTGATGAGCTTTGCTGTTCTCTCCACCTCTGCTGGCTGGGCGGCTGACTC
 AGCATCACCCCTCTGGGCTGATGTCCTCTCATCTTAAAGGACAAAGACATC
 TGAGATGATTCTACCCATCTGAGCAACAGGCTGACCTGCTCTGGGACT
 GTGGGAGACACCAACTTGCTCTTGGGCTCAAAAGTATGAGTGAAGATTCTTAAATTTC
 TCGCAGTCTCTGGAAAATATTCTTGGGCTGAGCAGCAAATCTGTAGGGATATCAGTGAAG
 GTCTCTCCCTCCCTCTGTTTTTTTTGGAGACAGAGATTGCTCTTGTCC
 CAGGCTGGAGTGTGATGGCTGATCTGGCTCACCAACCTCTGCCCTCTGGGCTAAGCA
 ATTTCTGGCTCTGGCTCACCAACCTCTGCCCTCTGGCTAAGCA
 ATTTTGTTTTAGTAGAGACAGGGTTCTCCATGTTGGTCAAGGCTGGCTCAAACTCCCA
 ACCTCAGGTGATCTGCCCTCTGGCTCCAGTGTGGATTACAGGTGTGAGGCCACTG
 TGCCGGGCCCTCCCTCTTGGGCTGAATACAAAGTAGAGAACACTTCTTCAC
 TGTGCTGAGAATTCTAGATACTACAGTCTTACTCCCTCTTGTATTCACTGTG
 ACCAGGATGGCGGGAGGGATCTGTCACTGTAGGTACTGTGCCAGGAAGGCTGGTGAA
 GTGACCATCTAAATTGCAAGGATGGTGAATTATCCCCTCATGTCCTAAATGGGCTTAACCTCT
 CTTGGCTTGAACACTCAACAGATCTAGGCCATCTGCTCTAACAGGTCTAAATCACTCAT
 CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCATTGCTGTGGTGTATCTGTGTT
 TCCCTGCTCTGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTGTTGTTGTT
 TCTGCTATTGTTGATCTGACCAAGTCCCTAAGTAGACAGAACATTCAACCTCTGGCTAGGATTGACA
 GCCTCTGTTTGTCTTACCAACATGTCTGAAATCTAACCTCTGGCTAGGATTGACA
 GTCATGGTGTGCTTATAAGCCAATAAATTCAATGTGAAAAAAAAAAAAAA

FIGURE 134

MRWILFIGALIGSSICGQEKFQGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEYAVTIEDLQALLDNEDEMQHNEGQERSSNNFNYGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKVRRPAVWLNAIHSREWI
SQATAIWARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVVDFIQKHGNFKGFIDLHSY
SQLLMYPYGVSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLLPANQTIPTAEETWLGLKTIMEHVRDNLY

Signal peptide:

amino acids 1-16

[REDACTED]

FIGURE 135

FIGURE 136

MASYLYGVLFAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP
SKDLTLKMGSAFLVKKELOLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGK
VVDDIIQGLDLTTAMVLVNHIFFKAKWEKFHLEYTRKNFPFLVGEQVTQVPMMHQKEQFAF
GVDTELNCFVLQMDYKGDAVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFI PRF
SISASYNLETILPKMGIQNAFDKNADFGSIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT
KFIIVRSKDGP SYFTV SFNRTFLMMITNKATDGILFLGKV ENPTKS

Signal peptide:

amino acids 1-20

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FIGURE 137

GGCTGACCGTGCTACATTGCCCTGGAGGAAGCTAAGGAACCCAGGCATCCAGCTGCCACGC
 CTGAGTCCAAGATTCTTCCCAGGAACCAAACACTAGGAGACAGCAGCTCTGGAAAGCACCG
 CCTTTATCTCTCACCTTCAGTCCCTTCTCAAGAATCCTCTGTCTTGCCTCTAAAG
 TCTTGGTACATCTAGGACCCAGGCATCTGCTTCCAGGCCACAAAGAGACAGATGAAGATGC
 AGAAAAGGAATAGTCTCTTATGTTGGTCTACTATTGCTATTAGAAGCTGCAACAAATTCC
 AATGAGACTAGCACCTCTGCCAACACTGGATCAGTGTGATCTCCAGTGGAGGCCACAGC
 CACCAACTCTGGTCCAGTGTGACCTCCAGTGGGTCAGCACAGGCCACCATCTCAGGGTCCA
 GCGTGACCTCCAATGGGTCACTGGGTCACTGGGTCAGCATAGTCACCAACTCTGAGTCCATACAACCTCCAGTGGG
 ATCAGCACACCCACCAACTCTGAGTTCAGCAGCGTCCAGTGGGATCAGCATAGGCCACAA
 CTCTGAGTCCAGCACACCTCCAGTGGGCCAGCAGGCCACCAACTCTGAGTCCAGCACAC
 CCTCCAGTGGGCCAGCACACCTCTGGTCCAGTGTGACCTCCAGTGGAGGCCAGC
 ACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCAGTGCACCAACTCTGA
 GTCTAGCACACTCTCCAGTGGGCCAGCACAGGCCACCAACTCTGACTCCAGCACACCTCCA
 GTGGGCTAGCACAGGCCACCAACTCTGAGTCCAGCACACCTCCAGTGGGCCAGCACAGCC
 ACCAACACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCAGTGCACCAACTCTGAGTCCAG
 CACAAACCTCCAGTGGGCCAGCACAGGCCACCAACTCTGAGTCCAGAACGACCTCCATGGG
 CTGGCACAGGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGCCAGCACAGGCCACAC
 TCTGACTCCAGCACAGTGTCCAGTGGGCCAGCACACTGCCACCAACTCTGAGTCCAGCACAGC
 CTCCAGTGGGCCAGCACGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGCCAG
 CAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGCCAGCACAGGCCACCAACTCTGAG
 TCCAGCACAGTGTCCAGTGGGATCAGCACAGTCAACCTGAGTCCAGCACACCCCTCCAG
 TGGGCCAACACAGCCACCAACTCTGAGTCCAGTAGCACCTCCAGTGGGCCAACAGCCA
 CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGCCAGCAGTGCACCAACTCTGAGTCCAGC
 ACACTCTCCAGTGGGTCAAGCAGGCCACCAACTCTGAGTCCAGCACACCTCCAGTGGGC
 TAGCACAGGCCACCAACTCTGACTCCAGCACACCTCCAGTGAAGGCCAGCACAGGCCACCAACT
 CTGAGTCTAGCACAGTGTCCAGTGGGATCAGCACAGTCAACCTGAGTCCAGCACAAACC
 TCCAGTGGGCCAACACAGCCACCAACTCTGAGTCCAGTAGCACCTCCAGTGGGCCAACAGCCA
 AGCACGCTGACTGGAATGCCACACAACACTTCCCATAGTCATCTACTGCACTGAGTGGCAA
 AGCCTGGTGGTCCCTGGCGTGGGAAATCTCCTCATCACCTGGTCTCGGTTGTGGCG
 GCCGTGGGGCTCTTGCTGGCTCTTCTCTGTGAGAAACAGCCCTGCCCCCTGAGAAAACAC
 CTTAACACAGCTGTCTACCAACCCCTCATGGCTCAACCATGGCTTGGTCAGGCCCTGGAG
 GGAAATCATGGAGCCCCCCCACAGGCCAGGTGGAGTCTTAACCTGGTCTGGAGGAGACAGTA
 TCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCCCTGAGCAGCCCCGGAAAGCAAG
 TGCCGCATTCTCAGGAAGAGAGACCTGGGCACCCAAGACACTGGTTCCCTTCATTCACTC
 CCAGGAGACCCCTCCACCTGGTGTGAGAATCTGAAAGAGGTATTCTCACC
 TTTCTGCCCTTACAGACACTGGAAAGAGAAATACTATATTGCTCATTTAGCTAAGAAATAA
 ATACATCTCATCTAACACACAGCACAGAAGAGAAGCTGTGCTGGCCCGGGTGGTATCTAG
 CTCTGAGATGAACTCAGTTAGGAGAAAACCTCATGCTGGACTCCATCTGGCATCAAAA
 TCTCCACAGAAAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAA

FIGURE 138

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAATAGCAGCGTGGCTCCCTGGCTCTCTGCATCCTCCGACCTTC
CCAGCAAT**ATG**CATCTTGCACGTCTGGTGGCTCTGCTCCCTCTGCTACTGGGGGCC
CTGTCTGGATGGGCGGCCAGCGATGACCCATTGAGAAGGTCAATTGAAGGGATCAACCGAGG
GCTGAGCAATGCAGAGAGAGGGTGGCAAGGCCCTGGATGGCATCACAGTGGAAATCACGC
ATGCCGGAAGGGAAAGTGGAGAAGGTTTCAACGGACTTAGCAACATGGGAGGCCACACCGGC
AAAGGAGTTGGACAAGGCGTCCAGGGCTCAACCCACGGCATGGACAAGGTTGCCATGAGAT
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTGGCATGGGTCAACAAACG
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC
CAGGCTGGGAAGGAAGCAGAGAAACTTGCCAAAGGGTCAACCATGCTGCTGACCAGGCTGG
AAAGGAAGTGGAGAAGCTGGCCAAGGTGCCAACCATGCTGCTGGCCAGGCCGGGAAGGAGC
TGCAGAATGCTCATAATGGGTCAACCAAGCCAGCAAGGAGGCCAACAGCTGCTGAATGGC
AACCATCAAAGCGGATCTTCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG
GGCCTCAGTCACACGCCCTTCATCAACCTTCCCCTGTGGAGGAGCGTCGCCAACATCA
TGCCC**TAA**ACTGGCATCCGGCTTGCTGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC
ATGACCTGGAGGGGTTGGGGTGGGGACAGGTTCTGAAATCCCTGAAGGGGTTGTACTG
GGATTGTGAATAACTGATAACACCA

FIGURE 140

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITAG
REVEKVVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGGGVNHAADQAGKEVEKLGGAHAAQAGKELQN
AHNGGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

FIGURE 141

FIGURE 142

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPLL L L L L L L Q P P P T W A L S P R I S L P L G S E E R P F L R F
E A E H I S N Y T A L L L S R D G R T L Y V G A R E A L F A L S S N L S F L P G G E Y Q E L L W G A D A E K K Q Q C S F K G
K D P Q R D C Q N Y I K I L L P L S G S H L F T C G T A A F S P M C T Y I N M E N F T L A R D E K G N V I L L E D G K G R C P
F D P N F K S T A L V V D G E L Y T G T V S S F Q G N D P A I S R S Q S L R P T K T E S S I N W L Q D P A F V A S A Y I P E
S L G S L Q G D D D K I Y F F F S E T G Q E F E F F E N T I V S R I A R I C K G D E G G E R V L Q Q R W T S F L K A Q L L C
S R P D D G F P F N V L Q D V F T L S P S P Q D W R D T L F Y G V F T S Q W H R G T T E G S A V C V F T M K D V Q R V F S G
L Y K E V N R E T Q Q W Y T V T H P V P T P R P G A C I T N S A R E R K I N S S I Q L P D R V L N F L K D H F L M D G Q V R
S R M L L L Q P Q A R Y Q R V A V H R V P G L H H T Y D V L F L G T G D G R L H K A V S V G P R V H I I E E L Q I F S S G Q
P V Q N L L L D T H R G L L Y A A S H S G V V Q V P M A N C S L Y R S C G D C L L A R D P Y C A W S G S S C K H V S L Y Q P
Q L A T R P W I Q D I E G A S A K D L C S A S S V V S P S F V P T G E K P C E Q V Q F Q P N T V N T L A C P L L S N L A T R
L W L R N G A P V N A S A S C H V L P T G D L L L V G T Q Q L G E F Q C W S L E E G F Q Q L V A S Y C P E V V E D G V A D Q
T D E G G S V P V I I S T S R V S A P A G G K A S W G A D R S Y W K E F L V M C T L F V L A V L L P V L F L L Y R H R N S M
K V F L K Q G E C A S V H P K T C P V V L P P E T R P L N G L G P P S T P L D H R G Y Q S L S D S P P G A R V F T E S E K R
P L S I Q D S F V E V S P V C P R P R V R L G S E I R D S V V

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGGAGGATGTGCACTGCAGCGCCGGCAGCGGCTACGAAGAGGACGGGGACAGGGCCGTGGAACCGA
 GCCCCAGGCCAGGGAGGACGGGGAGGGGGAGGG
 TGCGGGCCCCCGCTCCCGCCGGCAGGGGGAGGACGGCCGCCACCTCGCCGCCAGGCCGCTAGCGCGCG
 CGGGCATGGTCCCCTCTAAAGGCCAGGGCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
 CTCGGGGGGCGCTCGGGGGCCCGATGGGCGGCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
 CGGGCTAGGGGGGGCTGGCTCTCGTGGCGGGGGCAGCGGGCTGAGGGCGCGGGRCCTGCGGGCGGG
 GGGCCGG
 TGCTCGGGCTCTGCTGGGCTCTGCTGCTGCCCCGGCTTCAGGAGCTGAACGGAGCG
 GCCCCAGGG
 CGCATGG
 TCGTGGGAGTCATGACGCCAGAAAATACCTCGAGACTCGGGCGTGGCCGCTACAGAACATGGTCAAAGACAA
 TTCTGGGAAAATGTTCTCTCAAGTGAGGGGGTCTGACACATCTGACATTCCAGTAGTGGCCTACAGGG
 GTGTTGGGACACTCTACCGGCCCCAGAAAGATCTCTCATGATGCTCAAGTACATGCAACGACCAACTACTGGACA
 AGTATGAATGGTTATGAGAGCATGATGACCTGATCACAAAGAGGAGGGCTTGAGAGACTTCTGAGGGATT
 TGAACAGCAGGGGGCCCTCTTCTTCTGGGCAACAGACCTGGGCCCCAGGAAATAAAGGGAAATCTGGGCTCTGG
 AGCCTGGTGAAGAACTCTGATGGGGGGGCTGGCTGATCATGAGCCGGGGAGGTGCTTGGAGAATGGTGGCC
 ACATGGGCAAGTGTCTGGGGAGATGACACCCCATGAGGACCTGGAGGTGGAGGTGCTGGAGGTTG
 CAGGGGGTCACTGTGCTGTTATGAGATCGGCCAGCTTATGAGAAATTACAGGAGAACAAAAAGGGGG
 ACATATAGAGATCTTACACATAAAATCAGGAACTCATCACATACACCCAAACAAAACCCACCCCTTACAGT
 ACAGGCTTCAACAGGATCATGCTGGGGCAAGATATCAGGACCTCCGGCCATCGCACAAATACAGCTGCAACGGAAA
 TTGTCCTGATGAGCAAATACAGCAACACAGAAATCTAAAGAGGACCTTGAGGATCTGGAGAAATACTTGTATTGGCAG
 TTGAGGTTTCAAGGGCCAGGGAGGGAGGGAGGGAGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
 TTGAGGG
 TGGAGGATGATCATGACAAAGCCAGGAGGAGGGGGCATCTGGTCACTGGTCACTGGGAGGATCCAGTACGGCTACGGCC
 GGGTGAACCCCATGATGGGGCTGACTACATCTGGGACTCTGCTGCTCTGTTACAAAAGCACAAAGGGAGAAA
 TGACGGTCCCTCTGGGGAGGAGGG
 TGGATGACAAAGAGTGTGGGGCAAGGAATCATCAGGAATCTGGGATCTGGGACTCTGGCTTCTCTCAAAACTCTGAAGA
 AGCTGCTCCCTTCTAGCTGG
 TCCCTTCTGTCAGCTGGGTTCTGCTTCAACCTTGACTCACCAACCTGGACAAGGCAAAACAGTCTTACATGATGAT
 AGAACGCTCAAGCTGCTGGGTTCTGCTTCAACCTTGACTCACCAACCTGGACAAGGCAAAACAGTCTTACATGATGAT
 GAGATTCAGGGTAAAGTACCCATGGAGGATTTCTGGGAGGTGGCTGTTCTGGAGAGGTTTCAAGAGCCCTGG
 CCTTGGAGGTAGGATGATCTGGGCTTCAACATGAGTATTCTGGGAGGTGGCTGTTCTGGAGAGGTTTCAAGAGCCCTGG
 CAGAATTCTTCAAGGGATGTCGAGCAAATACAGTCTGGGCAACAAATATATTCTTCAACATCTCAGGCACT
 ATGACCCAAAGGATGTTTATAGGGAAAGTTCAGGAACTTCTCAGGAACTTCTGGCTTACTCAGGAAACACTGGCTCT
 GGAGAAACTATGGGATTTGGCACTTCAACATGCTGTTTATAGGGAGATCTGGCAGTGGGTGCTTGTGATTTCCA
 AGGAAGCTGGTGG
 AGGAAGTGGAGTGTGG
 GCTTGGGGTCAAGCATGACCTATGGGTCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAAATGATCCAA
 GTTACAGTAAAGCAGCAATAATTAATGCTGAGGAGGG
 TAATATTCTAATTATTCTTCAAAATTCTTGTGATGAGTTGTTGAGCTTGTGCTGATACAGGATAATTCTTAC
 AAGTGTGTTCTTACATAGGACTCTTCAAGTGTGCTTCTGAGGAAAGGTGATCAGTGTGCTTGTGCTTGTG
 CACATCTCTCTGGTCAACATTGACAGGCTGCTTAATCTGAGTAACTGTTGAGGAAATCTGATGAAACAAA
 TTAAAAAAATTTTCTGGACCCCTTGTGCTTCTGAGGAGGAAACCTGACACATTCTGCAAAACTT
 TATTGTAACAAAATTTCTGGTAAACTCTGGTAAATGCTGTTGATGTTGTTAACATTCACAGATTCTACCTTGT
 GTTTGTTTCTGGTAAACATTGTTTAAAGCCATTCTGCTTCAAGTGTGCTTGTGAGGAAAGACGCTT
 GCTGTTCTGATCATCTGCTTCAAGGAGGAGCTTCCAGGACTGATCATCTCTCTCATGTTACTCTGCTCACATGGC
 CACGGTAGGTTTGTGTTGTTGTTGAGGAGGAGCTCTGAGGAGGAGCTCTGACTCTCTGCTTACCCAGGGGG
 CAGTGGGGCAACTTGGCTCACTTAAACCTCCACCTTCCCTGGTCAAGCAATTCCCTGGCTTGGCTTCTCCGAGT
 AGCTGGGGATTACAGGACACACACCCACACCCAGGAGTGGTATTCTGAGGAGGAGCTTGGCTTCTCCGAGT
 GCAACGCGGCAACTTGGCTCAACACCCACACCCAGGAGTGGTATTCTGAGGAGGAGCTTGGCTTCTCCGAGT
 TGCTGGTACTCTGGGCTTAAATGAGCTGGCAATTAAAGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
 CTCTCTTAAAGGCTTAAATATTATGTTGAGATGACAAAGGATGAAATTCTACATTAATGATGACACAGACT
 GAAACATACACACACACACCCCAATCAAACAGTGG
 TTGTTATGTGGGGTGGAGATGGTTTCTTCAATTCTTCAACTGTTTGTGTTTACCTTGTGATTTGAGTGTGATCTG
 TTAAATTAATATCTGTTGAGGCTCTGCCATTCTGAGTACCTGTTGAGTGTGAGTGTGATTTGAGTGTGATCTG
 GAGTGTGTTTGTGTTTGTGAGTAAACCGATCTCAAGGATCTTGTGAAAGTCTTGTGAAACGCTTCTCCCTT

FIGURE 143B

TTAATTTTATATTCTTACTGTTTACTAAATAAGTGTTCTTGACAAATTGGTGCCTCATGTGTTGGG
GACAAAAGTGAATGAATCTGTCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTCCTTAATAATTGTT
TTCATTAGATTCAAACAGTGATAGACTTGCCATTAAATACACCTCATGGAGGGCTGCGTATTGTAAATAG
CCTGATGCTCATTGGAAAAATAAACCACTGAACAATTTCATTTCTATTGTACTTTCGAACCAATTGTCTCATT
ATTCCCTGTTTAGCTGAAGAATTGATTACATTGGAGACTAAAAACTTAAACACGGAAAAAA

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FIGURE 144

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRRAWLSVLLGLVLGFVLASRLVLPASELKAGRPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNLFVGVMTAQKYLQTRAVAAYRTWSKTI PGKVQFFSSEG
SDTSVPVIPVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRAADDVYIKGDRLENFLR
SLSNSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTIEHKEDLQLGIPPSFMRFQPRQREE
ILEWEFLTCKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRITDFKEIQY
GYRRVNPMPYGAEYILDLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFLSNSLKKLVPFQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESSLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPPIIFSQYDPKIVYSGKVPSDNHFAFT
QKTGFWRNYGFGITCIYGKDLVRVGGFDVSIQGWGLEDVDFNKKVVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

Signal peptide:
amino acids 1-23
```

FIGURE 145

GGACAACCCTGCTGGGTGTCAGGGCCTGAGGCAGGGTACTCCGCTGACACCTTCCC
 TTTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT
 ACGGACGACGCCTGAAGGCCCTAGTCCTCTAGTTGCGCTTTGCTATGGCCTTCGCTG
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACCTGAATCATTATATA
 CAAGTTTAGAGAACCTAGTAGAAGTGTCCCTCTGGGAGGCCAGTCGTGAGAAAAAAATC
 TAACTCTCAAAACATGTTATTCTATACCATCAAAGGGATCAAATTAAAGGAGCTAGTTA
 CACATGGAGACGCTTCAACTGAGAATGATGTTTAACCAATCCTATCAGTGAAGAAACTACA
 ACTTTCCCTACAGGGGCTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC
 ATTCTGGTCGATCAAACCAAAATGTTCCATTGTTGCATGCAGAGGAACCTTATATTG
 AAAATGAAGAGGCCAGAGCCAGACCCGGAGGCCAGTCGCAAAACAAACTGAGGCACCAAGAATG
 TTGCCAGTTACTGAATCATCTACAAGTCATATGTACACTACAGTCACCTGTCAC
 CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAACTCAGAAGATGTTCCCTCAGCTCT
 CAGGTGAAACTGCGATAGAAAACCCGAAGAGTTGGAAAGCACCCAGAGAGTTGGAATAAT
 GATGACATTTGAAAAAAATTAGATATTAAATTCAAGTGCAACAGGCACTTCTTAGTGA
 CACCAAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAACGAAGCC
 TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAACAATGTATAAGTCCAGTTATTGCCA
 GTAGGACGAACAAGTAATAAAATTGATGACATCGAAACTGTTATTACATGCTGTGTAATT
 TAGATCTAAACTCTATGAATATTAGATATTAAATGTTCCACCAGAGAGATGAGAGAAAAAG
 CTGCTACAGTATTCAATACATTAAAAAATTGTTGAGATCAAGGGAGAGTCACAGCCTTATT
 AAAGTTTATTAAACAATAATATAAAAATTAAACCTACTGATATTCCATAACAAAGCTGA
 TTTAAGCAAACCTGCACTTTTCACAGGGAGAATAATCATATTGTAATTCAAAAGTTGTAT
 AAAAATATTCTATTGAGTTCAAATGTGCCAACATCTTATGTGTCATGTGTTATGAACA
 ATTTCTATATGCACAAAAACCTAATTAAAATAAATTGGTTCAGGAAAAAA

FIGURE 146

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLLVALLLWPSSVPAYPSITVTPDDEEQNLNHYIQVLENLVRSPSGEPGREKKNSNSPK
HVYSIASKGSKFKELVTHGASTENDVLTNPISEETTFPTGGFTPEIGKKKHTESTPFWSI
KPNNVSIVLHAEepyIENEEPEPEPAKQTEAPRMLPVVTESSSPYVTSYKSPTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPEWNNDDILKKILDINSQVQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAEEHKLKTMYKSQLLPVGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPPMEMREKAATVFNTLKNMCRSRRVTALLKVY
```

Signal peptide:

amino acids 1-19

[1]
[2]
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FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCGCGCTGAGACAGCTGGCCTG
 ACCTCCAAATCATCCATCACCCCCCTCGTGTCACTCTGTTCTAGTGTGAGATCAACCCACA
 GGAATATCC**ATG**GCTTTTGTCATTGTTCTCAGTTTACAGGCTGGGAGGACGCCGTTCT
 GTGCAAGTCATGGACGGGCAAGTTGTCAGGCTTGGTGGGGAGGACGCCGTTCT
 CCTGCTCCCTTCTCCAGGACAGCTCAGAGGCTATGGAAAGTGCCTTCAGGAATCAG
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGAATCTAACGAGATGCCACA
 GTATCAGGGAGAACTGAGTTGTGAAGGACTCCATTGCAGGGGGCGTCTCTAAGGC
 TAAAAAACATCACTCCCTCGGACATCGGCTGTATGGGTCTGGTCACTCCCAGATTAC
 GATGAGGAGGCCACCTGGAGCTGCCGGTGGCAGCACTGGCTCACTTCTCATTTCCAT
 CGTGGGATATGTTGACGGAGTATCCAGTTACTCTGCTGCTCAGGCTGGTCCCCAGC
 CCACAGCCAAGTGGAAAGGTCACAAAGCAGAGATTGTTCTCAGACTCCAGAGAAATGCA
 GATGGGTACAGCTGTATGTTGAGATCTCATTATAGTCCAGGAAAATGCTGGGAGCAT
 ATTGTTGTCATCCACCTTGTGACGGAGACTGAGGGTGAATCCAACGTTATTGATAGGAG
 AGACGTTTCTCAGGCTTACCTTGGCTGGCTTCTATTACTCGGTTACTCTGTTG
 GCCCTGTGTGGTGTGATGGGATGATAATTGTTCTCAAATCAAAGGGAAAATCCA
 GGCGGAACTTGACTGGAGAGAACACCGGAGCAGGCAAGATTGAGAGAGGCCGAAACACG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTACCCGAAGCTCGGTTCTGATCTGAAA
 ACTGTAACCCATAGAAAACCTCCCAGGGTCTCAGGAGACATTACTGGGAGGTGGAC
 GAGTGTGGTGGCTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGAC
 AAAATGTAGGGTGTGGTATGTGGGAGTGTGCGGGATGACGAGCAGGGGAAAGAACATGTG
 ACTTTGTCCTCCAAACATGGGATTGGGCTCTCAGACTGACAAACAGAAATTGTTAC
 ATTCAATCCCCATTTCAGCCTCCCCCAGCACCCCTCTACACGAGTAGGGCTTCC
 TGGAATCTAGGGTGGGACCATCTCTTCTCAATAAATGACCAGTCCCTTATTATACC
 CTGCTGACATGTCAGTTGAAGGCTTGTGAGACCTATATCCAGCATGCGATGTAGCGA
 GGAAAAGGGACTCCCATATTCTATGTCAGTGTCTGGGAT**TGAG**CAGAGAAACCCCTG
 CTAAAGGGCCCACACAGACAGCCAGACACAGCCAAGGGAGAGTGCCTCCGACAGGTGGC
 CCCAGCTCTCTCGGAGCCTGCCAGAGACTGCCAGGCCCCAACTCTCTTGTAGGGAGC
 TGAGGTCTCTGCCCCAGGCTGCCAGAGCTGCCAGCAGCTTCCAGATGAGGGGGAT
 TGGCCTGACCTGTGGGAGTCAGAAGCCATGGCTGCCAGTGGTGAAGTGGGAGCGGAATAGACTCA
 CATTAGGTTTGTGAAGAAACTCCATCCAGCTAAGGGATCTGAACAAGTCACAAACCTCC
 CAGGCTCTATTGCTAGTCACGGACAGTGTCTCTGCTCAGGTGAAGAGTTAAGAGA
 CAACGAATGIAATCATGCTTGCAGTTGAGGGCACAGTGTCTGCTAATGATGTTTTA
 TATTATACATTTCACCATAAACTCTGTTGCTTACCTTACAGGTTGCTAATGATGTTTTA
 TACCAAAATCACCCTGGAATAGTTATGAAACACCTGCTTGTGAGGCTCAAAGAATAAAGAG
 GAGGTAGGATTTCAGTGTCTAAGGCCAGCATTACCTGATACCAAAACCCAGGCAAAG
 AAAACAGAAGAAGAGGAAGGAAACTACAGGTCCATATCCCTCATTAACACAGACACAAAAA
 TTCTAAATAAAATTTAACAAATTAAACTAAACATATTTAAAGATGATATAACTACT
 CAGTGTGGTTGTCCCACAAATGCAGAGTTGGTTAATATTAAATATCAACCAGTGTAAATT
 CAGCACATTAATAAAACTAAAAAGAAAACCATAAAAAA

FIGURE 148

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISTVGYVDGGIQLLCCLSSGWFQPQPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC
GVVMGMIIIVFFKSKGKIQAELDWRRKHGQAEELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGVYVGCRDDVDRGKNNVTLS
PNNGYWVLRITTEHLYFTFNPHFISLPPSTPPTRGVFLDYEGGTISFFNTNDQSLIYTLLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTCATCGTTGGCA**ATG**GATGTATCGGCCAGATGTGGTGGGGCTA
 GGAAAAGAGTTGGGGAAACCCGGTTATCGGCCCTCGTCATCTCATATCCGTATTGTC
 CTGGCAGTGTGCATTGGACTCACTGTCATTATGTGAGATATAATCAAAGAACCTACAA
 TTACTATAGCACATTGTCATTACAACGTGACAAACTATATGCTGAGTTGGCAGAGAGGCTT
 CTAACAATTACAGAAAATGAGCCAGAGACTTGAACTAATGTAAGGGTAAATGCAATTATAAA
 TCTCCATTAAAGGGAAAGAATTGTCAGACTCAGGTTATCAAGTCACTCAACAGAACATGG
 AGTGTGGCTCATATGTCAGTTGAGATTCACTACTGAGGATCCTGAAACTGTAG
 ATAAAAATTGTCACATTGTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCCTAAAGTA
 GATCCTCACTCAGTAAATTAAAAAAATCAACAAGACAGAACAGACAGCTATCTAAACCA
 TTGCTCGGAACACAGAACAGTAAACTCTAGCTCAGACTCTCAGGATCGTTGGGACAG
 AAGTAGAAGAGGGTGAATGCCCTGGCAGGCTAGCCTCAGTGGGATGGGAGTCATCGCTG
 GGAGCAACCTAATTAAATGCCACATGGCTTGAGTGTGCTCACTGTTTACAACATATAA
 GAACCCCTGCCAGATGGACTGCTCCTTGGAGTAAACAATAAACCTCGAAAATGAAACGGG
 GTCTCCGGAGAATAATTGTCATGAAAAAATACAAACACCCATCACATGACTATGATATTCT
 CTTGCAGAGCTTCTAGCCCTGTTCCCTACACAAATGCACTGACATAGAGTTGTCTCCCTGA
 TGCATCCTATGAGTTCAACCAGGTGATGTGATGTTGTGACAGGATTGGAGCACTGAAA
 ATGATGGTTACAGTCAAATCATCTCGACAAGCACAGGTGACTCTCATAGACGCTACAACT
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCTAGAATGTTATGTGCTGGCTCCTT
 AGAAGGAAAAACAGATGCATGCCAGGGTGACTIONGGAGCCACTGTTAGTCAGATGCTA
 GAGATATCTGGTACCTGCGGAATAGTGAAGCTGGGAGATGAATGCGAAACCCAACAAG
 CCTGGTGTATTAATAGAGTTACGGCCTGGGGACTGGATTACTCTAAAAACTGGTAT**CTA**
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTGTTTTGGGTGTGGAGGCCATT
 TTTAGAGATAACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTCAATAAAC
 TGTGTTGCTTGATGCATGTATTCTTCCAGCTGTTCCGCACGTAAGCATTGCTTCTG
 CCAGATCAACTCTGTCATCTGAGCAATAGTGAACATTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCAATTGTTCTAGAAGTTGTCAAGATTGAC
 TTGTTGACATAAATTGTAATGCATATACAAATTGAGCTCCTTCTCAGTTCTC
 AGCTCCTCTCATTTCAGCAAATATCATTCAAGGTGAGAACAGAGGTGAAAGAAAATA
 TAAGAAGAAAAAAATCCCCTACATTATTGGCAGAAAAGTATTAGGTGTTTCTTAGT
 GGAATATTAGAAATGATCATATTCAATTGAAAGGTCAAGCAGAACAGCAGAACATCAAC
 ACTTCATCATTTAGGAAGTATGGGAACTAAGTAAAGGAAGTCCAGAAAGAACAGAACATATA
 TCCTTATTTCATTCCAAACAACTACTATGATAAAATGTGAAGAAGATTCTGTTTTGTG
 ACCTATAATAATTACAAACTCATGCAATGTAATTGTTCTAAGCAAATTAAAGCAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAAATAATCACCAC

FIGURE 150

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAYKSPRLREEFVKSQVIKFQQKHGVLAHMLLICR
FHSTEDPETVDKTVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPFSDYDISLAELOSSPVYTNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

GTCGAAGGTTATAAAAGCTTCCAGCAAACGGCATTGAAGGTGAAGATAACAACCTGACAGCA
 CAGCCTGAGATCTGGGGATCCCTCAGCCTAACACCCCACAGACGTAGCTGGTGGATTCCCG
 CTGCATCAAGGCCAACCCACTGTCTCCATGCCTGGCTCTCCCTGCCTCTGTGGCTCTGGC
 CGTGACCTTCTGGTTCCAGAGCTCAGGCCCTTGCCCCCTCAAGACTTGAGAAAGAGGAGG
 CAGATGAGACTGAGACGGCGTGGCCGCCCTTGCGGCTGTCCCTGCGACTACGACCACGTG
 CGCACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTGGGCCGCCCTGCCCTGTGCC
 AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCATGGGAGAAGTGCGCATTGCG
 CCCAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCTCTCCCCGGTCCACTACTGG
 CTGCTGCTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCGCTGAACGCTACGGTCCG
 CAGAGCGCACTGAAGGGCTGAAGCCAGGGGATTATGCTGTTGGTAGTGGCGCTA
 ACGAGGCCGGGCAAGCCGCGTGGCCCAAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC
 CCTGCCCTGGGCTTGCAGCCGCCCTGCGGTGCCCCAACCCCCCCTCTGGTCCACGC
 GGCGTCGGGTGGCACGGCCCTGCCCTGCTAACGCTGTGCCGCCCTGGTGTGGCACTTCT
 GCCTGCGCGATCGCTGGGCTGCCGCCGAGCCGCCCGAGCCGAGGGGCCCTTGA
 AAAGGGCCTGGGGCATCTGGGACAGACAGCCCCACCTGGGGCGCTCAGCCTGCCCG
 GGAAAGAGAAAACCGCTGCCCTCAGGGAGGGCTGGACGGCGAGCTGGAGGCCAGCCCCAG
 GCTCCAGGGCACGGCGAGTCATGGTCTCAGGACTGAGCGCTTGTAGGTCCGGTACTT
 GGCCTTGTCTGGCTAGGTCTGGGAAGGAATAAGAAAAGGGCCCCAATTTTTTTTA
 AGCGGCCAGATAATAATGTAACCTTGCCTTGGTTAAAAAAAAAAAAAA

FIGURE 152

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRHLQVPCKE
LQRVGPAACLCPGLSSPAQPPDPPRMGEVRIAEEGRAVVHWCAPFSPVLHYWLLWDGSEA
AQKGPPLNATVRRAELKGLKPGGIYVVCVVAANEAGASRVPQAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVHAAVGVGTALALLSCAALVWHFCLRDRWGCPRRAAARAAGAL
```

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGAGAAAAGACGCTCCAGCTGAAGCCAATGCAGCCCTCGGCTCTCCGCGAAGAAGTTCC
 CTGCCCCGATGAGCCCCCGCCTGGCTCCCGACTATCCCGAGGCGGGCGTGGGCACCGGG
 CCCAGCGCCGACGATCGCTCCCGTTTCCGCTTGGAGTAGGATCTGGTAAAGGATGGGG
 TTCTCCCTAACGGGCTACA**ATGGCCAGAGAAGATCCCTGAA**GTCTGCGCTGCTGCT
 CTACGCCCTAACATCTGCTCTTTGTTAATGTCATCAGTGTGTTGGCAGTTCTGCTTGG
 TGAGGGACTACCTAAATAATGTCATCTTAACTGAGAAAACGAGGGTAGAGGAAGCAGTC
 ATTTGACTTACTTCCGTGGTTCATCCGGTCAATGATTGCTGTTGCTGTTCCCTATCAT
 TGTGGGGATGTTAGGATATTGGAACGGTAAAAAGAAATCTGTTGCTTGTGATGGTACT
 TTGGAAGTTGCTGTCATTTCTGTTAGAATGGCTGTGGCGTTGGACATATGAAACAG
 GAACATTATGGTCCAGTCAATGGTCAGATATGGTCACTTGGAAAGGCCAGGATGACAAATT
 TGGATTACCTAGATATCGTGGCTTACTCATGCTGGAAATTTTCAAGAGAGACTTAAAGT
 GCTGTGGAGTAGTATATTCACTGACTGGTGGAAATGACAGAGATGGACTGGCCCCAGAT
 TCCGTGTTAGAATCCCGAGTTTCAAAACAGGCCCCACCAAGGAAGATCTCAGTGA
 CCTTTATCAAGAGGGTTGGGAAGAAAATGATCTTCTGGAGAGGAACCAAACACTGC
 AGGTGCTGAGGTTCTGGGAATCTCATTGGGTGACACAAATCTGGCCATGATCTCACC
 ATTACTCTGCTCTGGCTCTGATTATGATAGAAGGGAGCTGGGACAGACCAAATGATGTC
 CTGGAAAGAATGACAACCTCAGCAGCTGTCATGTCCTCAGTAGAAGTGTGAAACCAAGCC
 TGTCAAGAATCTTGAAACACATCCTGGCAACAGCTTAAACACACTTGGAGATGGAG
 GAGTTA**TAAA**AAGAAATGTCACAGAAGAAAACCACAAACTGTTTATTGGACTGTGAATT
 TTTGAGTACATACTATGTTTCAGAAAATGTAAGAAAATTTGCTGCTAAATAAACAA
 CTTAAGCATATACTATCTCATGCTTAAAGATGAGGATGGAAAAGTTGCTATGTCATAAGTCAC
 CACCTGGACAATAATTGATGCCCTTAAAGTCAGTAGAAGACAGATGTCATACCCACTGTTGAGC
 CTGTTGATGACTTTTACTGAAACACAGTTGTTGAGGCAGCATGTTGATTAGCATTTC
 CGCATCCATGCAAACGAGTCACATATGGGGACTGGGCCATAGTAAGGTTGATTACTT
 CTACCAACTAGTATATAAAGACTAATTAAAGCTAACATAGGAAGTTAGAAAATACTAATA
 ACTTTTATTACTCAGCGATCTTCTGATGCTAAATAATTATATATCAGAAAATTT
 AATATTGGTGAACCTAAATGTTGATTTGCTGGTACTAAATAATTCTTACCCACTTAAA
 GAGCAAGCTAACACATTGCTCTTAAGCTGATCAGGGATTTTGTTGATATAAGTCTGTTAAA
 TCTGTTAATTCTAGTCGATTCAGTTCTGATAATGTTAAGAATAACCAATTATGAAAAGGAAA
 ATTTGTCCTGTTAGCATCATTATTTAGCCTTCTGTTAATAAGCTTTACTATTCTG
 CCTGGGCTTATATTACACATAACTGTTATTAAATACTAACCAACTAATTGAAAATT
 CCAGTGTGATACATAGGAATCATATTAGAATGTTAGCTGGCTTCTAGGAAGTTAATAAA
 GAAAATTGCAACATACTTAGTGATTCAAGAAAGGACTGTATGCTGTTTCTCCAAATG
 AAGACTCTTTTGACACTAAACACTTTTAAAAGCTATCTTGCCTTCTCCAAACAAAGAAA
 GCAATAGTCTCAAGCTAACATTAAATCTACAGAAAATAGTGTCTTTCTCAGAAAAT
 GCTTGTGAGAATCATTAAACATGTGACAATTAGAGATTCTGTTTATTCTACTGATTA
 ATATACTGTGCAAAATTACACAGATTAAATTAAATTGTTTACAAGAGTATGTTATTT
 GAAATGGGAAAGTCGATTACTGTTGTTGTTGTTATTCTCAGAATATGGAA
 AGAAAATTAAATGTGTCATAAAATTCTAGAGAGTAA

FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAWSAWMRDYLNNVLTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMNTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMWDPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFGLGISIGVTQILAMILTITLLWAL
YYDRREPGBTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTGCTCAGCGGACAAGGATGCTGGCGTGAGGGACCAAGGCCCTGCC
 TGCACTCGGCCCTCCAGCCAGTGCAGCAGGACTCTGACCTGCTGGCCAGCCAGGA
 CCTGTGTGGGGAGGCCCTCTGCTGCCTTGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
 ACCGGGAGGATCACAGAGCCAGCATTACAGGATCTGACAGTGAACACTCTGAACAGC
 CTCGATGTCAAACCCCTGCGCAAACCCGTATCCCATGGAGACCTTCAGAAAGGTGGGAT
 CCCCATCATAGCACTACTGAGCTGGCAGATCATCATTGTGGTGTCTCATCAAGG
 TGATTCTGGATAAATACTACTTCCTCTGGGGCAGCCTCTCCACTTCATCCCAGGAAGCAG
 CTGTGTGACGGAGAGCTGAGCTGCCCTGGGGAGGACGAGGAGACTGTGTCAAGAGCTT
 CCCCGAAGGGCCTGCACTGGCAGTCCGCTTCCAAGGACCGATCCACACTGCAGGTGCTGG
 ACTCGGCCACAGGAACTGGTTCTCTGCCTGTTGCACAACCTCACAGAACGCTCTCGCTGAG
 ACAGCCTGTAGGCAGATGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGA
 TGTGTGAAATCACAGAAAACAGCCAGGAGCTCGCATCGGAACCTCAAGTGGGCCCTGTC
 TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTGCCTGTGGGAAGAGCTGAAGACCCCCG
 GTGGTGGGGAGGAGGGCTCTGTGGATTCTTGGCCTTGGCAGGTAGCATCCAGTACGA
 CAAACAGCACGTCTGTGGAGGAGCATCTGGACCCCCACTGGGTCTCACGGCAGCCACT
 GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGGCAGGCTCAGACAAACTGGG
 AGCTTCCCACATCCCTGGTGTGGCCAAGATCATCATCATTGAATTCAACCCATGTACCC
 AGACAATGACATCGCCCTCATGAAGCTGCAGTCCCACACTTTCTCAGGCACAGTCAGGC
 CCATCTGTCTGCCCTCTTGATGAGGAGCTCACTCCAGCCACCCACTCTGGATCATGG
 TGGGGCTTACGAAGCAGAATGGAGGGAGATGTCTGACACTACTGTCAGGCAGTCCA
 GTCATTGACAGCACACGGTCAATGCAAGCAGATGCCATTACAGGGGAAGTCACCGAGAAGA
 TGATGTGTGCAAGGCATCCCGAAGGGGTGTGGACACCTGCCAGGGTACAGTGGGGCC
 CTGATGTACCAATCTGACCACTGGCATGTGGTGGGATCGTTAGCTGGGGCTATGGCTGCG
 GGGCCCGAGCACCCAGGGATACACCAAGGTCTCACGCCACTCTCAACTGGATCTACAATG
 TCTGGAAGGCTGAGCTGTAATGCTGCTGCCCTTGCAGTGCAGTGGAGGCCGCTTCC
 CCCTGCCACCTGGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTGGTACACCC
 CTCTGCCACAGCCTCAGCATTCTGGAGCAGCAAAGGGCTCAATTCTGTAAGAGACCC
 TCGCAGCCAGAGGCGCCAGAGGAAGTCAGCAGGCCACTGCTCGGCCACACTGGTGTCCC
 AGCATCCCAGGGAGAGACACAGCCACTGAACAAGGTCTCAGGGTATTGCTAACGCAAGA
 GGAACCTTCCCACACTACTGAATGGAAGCAGGCTGTCTGTAAAGGCCAGATCACTGTGG
 CTGGAGAGGAGAAGGAAAGGGTCTGCCAGCCCTGCGTCTCACCCATCCCCAAGCCTA
 CTAGAGCAAGAAACCAGTTGAATATAAAATGCACTGCCACTGTTGGTATGACTACCGTT
 ACCTACTGTTGTCAATTGTTATTACAGCTATGCCACTATTATAAAGAGCTGTAAACATCT
 CTGGCAAAAAAA

FIGURE 156

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIALLSLASIIIVVVLIKVILDKYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAAETACRQMGYSRAVEIGPDQDLDVVEITENSQELMRMRNSSGPCLSGSLVSL
HCLACGKSLKTPRVVGEEAVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDV
FNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDTCCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKEL

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGGCTGAGGCACTGAGAGACCGAAAGCCCTGGATTCCAGAGGGAGGGAAACGCAGGGCATCCCCAGGCTCCAG
 AGCTCCCTGGTACAGTCGTGGCTGAGCATAGGCCCTCCAGCCCTGGCTGGACCCCTGGAGCCTCTGGGCC
 TTTTCCCTTCAACTGCTTCACCTGCTGCTGCCAGCACGCCGGGGAGGCCAGGGCCATGCCA
 GGGTCAGATACTATGCAGGGATGAACGTAAGGCCACTTAGCTTCTCCACCAAGAAGGCCCTCCAGGATTTGACA
 CTCTGCTCTTGAGTGGTGTGGAAATACTCTCTACAGTGGGGCTGGAGAACGCACTTCTGGCCTTGGATATCCAGG
 ATCCAGGGTCCCCAGGCTAAAGAACATGATACGGCCAGCAGTACAGAAAAAGAGTGAATGTGCCTTAA
 AGAAGAACAGCAATGAGACACAGTGTTCACATTCACTCGTGTCTGGTTCTTACAATGTACCCATCTTACA
 CCTGGGGCACCTTCGCCCTCAGGCCCTGCTGTACCTTCATGAACTTCAGAATTCTACCTGTCGCCATCTCGG
 AGGACAAGGTATGGAGGGAAAGGCCAAAGGCCCTTGACCCCGCTCACAGCATAAGGCTGTCTGGTGGATG
 GGATGCTCTATTCTGGTACTATGAAACAATTCTCTGGGAGTGGCCATCTGTAGCGCACACTGGGATCCAGC
 CTGTCTCAAGACCACAACTTCTCCGCTGGCTGATCATGACGCCCTCTTGTGGCAGCCATCCCTCGACCC
 AGGTGCTACTTCTTCAGGAGACGCCACCGAGTTGACTCTTGAGAGGCTCCACACATCGGGTGG
 CTAGAGCTGCAAGAATGACGTGGGGCGGAAAGCTGCTGAGAACAGTGGACACCCCTCTGAAAGGCCAGC
 TGCTCTGACCCAGGGGGCAGCTGCCCTTCAGCTTCACCTGAGCTCCAGGCCACGGCTCTGCTCCCGCCGATCTCCCA
 CAGCTCCCACATCTACGAGCTTCACCTCCAGGGCTGGAGCTGGGGGACCCAGGAGCTCGGGTTTGTGGCT
 TCTCTCTTGAGACATTAGCTGCTTAAAGGCAAATAAACAGTGTAAACAAGAAACTTACGCTGGACTA
 CTTATAGGGCCCTGAGACCAACCCCGGCCAGGCTGCTGAGTGGCCCTCTCTGATAAGGCCCTGACCT
 TCATGAAGGACCATTCCTGATGGATGAGCAAGTGGGGAGCCCTGCTGGTAAATCTGGCTGGAGATATA
 CACGGCTGAGTGGAGACAGCCAGGGCTTGAGGGCACAGCCTCTGTGATGACCTGGGAAACACCACAG
 GGTGCTCCACAGGCTGTGGTAAGTGGGACAGCAGTGTCACTGGTGGAAAGAGATTGAGCTGTCTGGTACCC
 CTGAACTCTTCGCAACCTGCACTGCTGCCACCCACCGGGTGCAGTGTGTTAGGCTCTCAGGGAGTGTGGA
 GGGTCCCCGACCCAACTGTAGTGTCTATGAGAGCTGTGGAGACTGTGTCTTGGCCGGACCCCACTGTGCT
 GGGACCCCTGAGTCCCAGCTGTGCTCTGTCTGCCCTTGGGAAACCTGTAACCTGGAGCAGGACATGGAGCCGG
 GGGACCCAGAGTGGCATGTGCACTGGGCCCCATGAGCAGGACCTGGGCTCAGAGCCCGCCAAATCATTA
 AAGAAGTCTGGCTGTCCCCAACCTCATCTGGAGCTCCCCCTGCCACCTGTCACTGGCTTGGCTTATTATT
 GGAGTCATGGCCAGCAGCAGTCCAGAACGCTCTTCACTGTCACATGCTGCTGATAGTCAGG
 ATGGAGTTGGGGTCTCTACCTGCTGGCAACTGAGAATGGCTTTCATACCTGTCATCTCTACTGGTGG
 ACAGCCAGGACCAAGACCTGGCCCTGGATCTGAACGGCAGTCACCCGGGAGCATGTAAGGTCCTGTTGA
 CCAGGGTCAGTGGTGGGCCGCCCTGGCTGCCAGCAGTCTACTGGCCCACTTGTCACTGTCACTGCTCT
 TTGCTTGTGCTTCAAGGAGCCCTCATCTCTGCTGCCCTGGGAGAGGAGCTGGCTGCCCTGGGCAAGG
 TTCAGGGCTGTGAGACCCCTGCCCTGGGAGAGGAGCTGGCTGAGCAGAGCACACCTCCAGTCTCCAAAGG
 AATGAGCAGGACCTCTGGCAGTGTGGAGCTGACACAACACTGGCTAGGACTGAGGTAGCTTAACTCTAGGCA
 CAGGCCGGGCTGGCTGGGAGCTGGGAGCTGGGAGCTGGCTGGGAGCTGGGAGCTGGAGAGCAG
 CAGCACAAAAGACCACTTCTCCCTGAGAGGGAGCTGTGACTCTGTCATCACTGATGACACTCAGCAGGGT
 ATGCACAGCAGTCCTCCCTCCCTATGGACTCCCTTACCAAGACCATGAGCTCTTAACAGGGTGGGGTAC
 CCCAGACCTGCTCTACACTGATATTGAGAACCTGGAGAGGATCTTCAGTCTGGCATTCCAGGGACCCCTC
 CAGAACACAGTGTTCAGAGACCCATAAAACCTGCCCTGCCAGGACCCATGGTAATGAAACACCAACATC
 TAAACAAATCATATGCTAACATGCCACTCTGGAAACTCCACTGAGAGCTGCCGTTGGACACCAACACTCCCT
 TCTCCAGGGTCACTGCCAGGGATCTGCTCCCTCTGCTTACAGTGTGACCCCTGACTCCAGGAAAGTC
 TTCTCTGAAGTGTGACCCATTCTCTTCTGCTTCAAGTGGGAGACTCTGATCCCTCTGCCCTGGAGAATGG
 CAGGGGAAATCTGAGCCTTCTCACTCCCTTACCTAGCTGACCCCTCACCTCTCCCTTCTGGGTTTGTG
 TTTGGGATTCAAGAAAAGCTGCTGTGAGAGACTGTTTATTATTAAGGCTTAAAAAA

FIGURE 158

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYYAGDERRALSFFHQKGLQ
DFDTLLLSDGNTLYVGAREAILALDIQDPGVPRLKNNMPWPASDRKSECAFKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLPISEDKVMEKGQSPFDPAHKHTA
VLVDGMLYSGMTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFF
ETASEFDFFERLHTSRVARVKNDVGGEKLLQKKWTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NFRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLV
YLGTTTGSLLHAKVVGDSAAHLVEEIQLPDPPEPVRLNQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCWDPESTCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP
QSRPQIIKEVLAAPNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQLALDPELAGIPREHVKVPLTRVSGGAALAAQOSYWP
HFVTVTVLVLFALVLSGALIILVASPLRALRARGKVQGCETLRPGEKAFLSREQHLQSPKECRT
SASDVEDADNNCLGTEVA
```

Signal peptide:
amino acids 1-30

Transmembrane domains:
amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTAGCCGGCGCAGGGCGCGAGCCCAGGTGAGATCCGGGCTTCGTAGAAG
 TGAGC**ATGG**CTGGGAGCAGTGCTCTCTAGTGGGCTCCTTCCTGGGTCTGCTC
 TCAGAGGCTCCAAAATCTGACAAATATCTACAGTAGGTGAAAGCCATTATCTACTGATGGA
 CCGGGTTCTCAGATTCTCAAGATCACGGTATAATGTCACCATGCTAACACAAAAGAG
 GTCTTTATGCCAGATTTAAAAGAAGAAAATCATATCAAGTATCAGTTGGCTTGCA
 CCTGAAGATCATCAAAGAGAATTTAAAAGAGTTGATTTCTGGAAAGAAAACCTTAGG
 TGGCAGAGGAAATTGAAAACTTAAATGTTAGAATACTTGGCTTGCACTGCAGTC
 ATTTTTAAAGAAGGATATCATGGATTCTTAAAGAATGAGAACATTCGACATGGTATA
 GTTGAACATTGACTACTGTCTTCTGATTGCTGAGAAGCTTGGGAAGGCATTGTC
 CATTCTTCACTTCACTGGCTCTTGGAAATTTGGCTACCAATCCCTTGTCTTATGTC
 CAGTATTCCGCTCTGCTGACTGATCACATGGACTCTGGGCCAGTGAAGAATTCTG
 ATGTTCTTCTAGTTCTGAGGAGGCAACAGCACATGCACTACATTGACAACACATCAA
 GGAACATTTCACAGAAGGCTAGTGGCAGTTTGTCTACCTCTACTGAAAGCAGAGTGT
 GCTTCATTAACTGACTTGTCTTGTGTTGCTGACCTCTGCTTCCAACACTTTAT
 GTTGGAGGCTGTGAAAAACCTATAAACAGTACCCAAAGACTTGGAGAACCTGCATTG
 CAAGTTGGGACTCTGTTGTCTTGTCTGACCTGGCTCCATGTTGAACACCTGTCAGA
 ATCTGGAAATCTCAAGGAGATGAAACATGCTTGTCTACCTACCCCAAGGGGTGATATGG
 AAGTGTCACTTCTCATGGCCCAAGATGTCACCTGGCTGCAATGTGAAATGTGGA
 CTGGCTTCCCTCAGAGTGACCTCTGGCTACCCAAAGCATCCGTCGTGTTGTACCCACGGC
 GCGACAATGACATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGATCCTCTCTT
 GGAGACAGCCGTGAAAACATGGTCCAGTAGAACGCCCCAAAGTTGGTCTTCTATTCAGTT
 AAAAGCTCAAGGCAGAGACATTGGCTTAAAGATGAAACAAATCATGGAAGACAAGAGAT
 ACAAGTCCGGCGCAGTGGCTGAGCTGTCTGCTCCACCCGCTCAGCCCCACACAG
 CGGCTGGTGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCAGCACCCTAACGCC
 TGCTTCTACCGACGCCCTGCCATGAGCAGTACCTCTGCGACCTTTTGTTCTGCTGGGG
 TCACTCTGGGACTCTATGGCTTGTGGAGCTGCTGGCATGGCTGTCTGGTGGCTGCGT
 GGGGCCAGAAAGGTGAGGAGACA**TAAG**GGCAGGTGACGCCCTGGGGGCTGTGTTGGTGG
 GCGATGTCACCATTTCTAGGGAGCTTCCACTAGTTCTGGCAGCCCCATTCTCTAGCTCT
 TAGTTATCTCTGTTCTGAGAACAGGAAAATGCCAAAATCATCTTCACTTGC
 TAATTTGTACAAATTCTCTTACTAGCTCTGCTGCTAGCAGAAATCTTCCAGTC
 CTGCTCTCCCTTGTGCCATCAGCAAGGCTATGCTGTGATTCTGCTCTGAGTGACTTG
 GACCACTGACCCCTCAGATTCCAGCTTAAATCCACCTTCTCTCATGCGCTCTCCGAA
 TCACACCCCTGACTCTCCAGCCTCATGTCAGACCTAGTCAGCCTCTCTCACTCTGCC
 TACTATCTATCATGGAATAACATCCAAGAAAAGACACCTTGCATATTCTTCAGTTCTGTT
 TGTCTCCACATATTCTCTCATGCTCAGGAAGGCTGCCCTGTGCTTGAGAGTTGAGG
 CGGACACAGGCTCACAGGTCTCACATTGGGCTCTGTCTGGTGCCACAGTGAGCTCC
 TCTGGCTGAGCAGGAGACTGTAGGTTCCAGATTCTCTGAAAGAAAATAAAAGTTACA
 CGCTTATCTCCCCAACCTCACTAA

FIGURE 160

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169
><subunit 1 of 1, 523 aa, 1 stop
><MW: 59581, pI: 8.68, NX(S/T): 1
MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGP
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPPIPLSYVPV
FRSLLTDDHMDFWGRVKNFIMFFSFCRRQQHMQSTFDNTIKEHTEGSRPVLSHLLLKAELWF
INSDFAFDARPLLPTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLSMVNTCQNP
EIFKEMNNAFAHLPQGVVIWKCQCSHWPKDVLAAANVKIVDWLPQS DLLAHPSIRLFVTHGQ
NSIMEAIQHGVPVMVGIPPLFGDQOPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPPLSPTQRLVGVIDHV LQTGGATHLKPYVFQQPWEQYLFDVFVFLGLT
LGTLWLCGKLLGMMAVWWLRGARKVKET
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTGTGGGGATTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
 GCCTCTGGCATATGCACACACTCACACACATCTGTCAACACCCGTCAACACACATACATGTT
 CTCCATCCCCCAGGTCCAGGCCCTCACTGTCTCCCACAGCAGGGTACCCCTGAAGCTCT
 GGCTGCAGCCCTCCCGTCAGTGGCAGGGCTTCATCCCTCTTCTCTCCAAAGCCCA
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGAACTGCAGTGACAGCAGGAGTAAGAGT
 GGGAGGCAGGACAGAGCTGGGACAGAGTATGGAGAGGGGTTCAAGCAGGCTAGAGAGGGC
 AGACTATCAGGGTGCGGGGTGAGAACATTCAGGGAGAGGAGCGGAAACAGAAGAGGGCAGA
 AGACCGGGGCACTTGTGGGTCAGAGCCCTCAGCAATGTTGGGAGCCAAGCCACACTGGC
 TACCAAGGTCCCTACACAGTCCGGGCTGCCCCCTGGTTCTGGTGCTTCTGGCCCTGGGGCC
 GGGTGGGCCAGGAGGGGCTAGAGGCCGCTCTGCTGGAGGGGAGTGCCCTGGTGTGTGA
 GCCTGGGCCAGGACTGCGAGGGGGGGGGGGGGAGCAGGCCCTGGAGAGGCACCCCTGGG
 GAGTGGCATTGCTGCCGCCGAAGCCACCCATGAGCCAGCAGGGAAACCGCAATGGC
 ACCAGTGGGCCATCTACTGCCAGGCTCTGTGAGCCAGGGGCGGTGGTGGACGGG
 CTCTGGCTCTTGTAGCCCCCTGTCCCCGGGTGTACAGCTCCGGTTCATGTGTTGAGG
 TGTAACAACGCCAAACTGTCAAGGTGAGGCTGATGCTGAACACAGTGGCTGTATCTCAGCC
 TTGCAATGATCTGTGAGCTGACGGCAGGCCACAGCAGCTCTGTGCTACTGCCCCGG
 CCGTGGGGACCGAGGTGTGCGCTGCCGTGAGGGAAATCTAGGGGTTGGAAATACT
 CAAGTTCTCTGGCTCTCATCTTCTCTTGAGGAAACCAAGTCTTCAAGCACAGAAAT
 CCAGCCCCGACAACCTTCTGCCCTCTTGGCCAGAAACAGCAGAGGGCAGGAGAGG
 ACTCCCTCTGGCTCTCATCCACCTCTTGTGATGGGACCCCTGTGCAAACACCCAAAGTTAA
 GAGAAGTGAAGTGAAGCTGTGGCATCTCCAGACCCAGGCTTCTGGCCACCCACCC
 CTCCCAGGCCACCTGTGCACTGTCTGGCTCTGAGCCCTAGGATCAGGGCAAGGTTGGCA
 AGAAGGAAGATCTGCACTTGTGCGCTCTGCTCTCCGGTTCCCCCACCCAGCTTCC
 GCTCAATGCTGATCAGGGACAGGTGGCAGGTGAGCTGACAGGGCCCCACAGGGCCAG
 ATGGACAAGGCTCAGCGTACCCCTGCAGGGTCTCTGGTGAAGGAAAGCCAGCATCAGGATC
 TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGCTAGGGTGGAGGCTAGCCAC
 AGCCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAAGGAAGGGAGGGTGTATTG
 TCTAGACTGAACATGGTACATCTGGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
 GGCTGTCTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
 GGTGAGTGTGTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATAAGAGCTGGAAGTG
 ACCATGGAAAACATCGATAACCATGCACTCTTGTGCTGGCCACCTCTGAAACTGCTCCAC
 CTTGAAAGTTGAACTTGTGCTCTCCACACTCTGACTGCTGCCCTCTCTCCACCTCTC
 TCACTGAGTTATCTCACTGTACCTGTGCTGCCAGCATATCCCACATCTCTCTCTGAT
 CTGTGCTGTCTTATTCTCTCCCTAGGCTTCTCTTACCTGGGATTCATGATTCACTCCT
 CAGACCCCTCTGGCAGTGTGCTAAACCCCTCCCTCTCTTCTTATCCGCTGCTGCTG
 GGCCAGGCTGGATGAATCTCAATAAAACAATAGAGAATGGTGGTCAAGGTACAAGTAGGT
 AGAATTACTAAGGAGAAGATGCCCTGGAGTTGGATCGGGTGTACAGGTACAAGTAGGT
 TGTTGCAAGGAAAATAATCAAACATGTATACTAAATTAAAAAA

FIGURE 162

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGLHSPGLPLVLLALGAGWAQEGSEPVILLEGECLVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVVKVYNRQTVQVSIMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL

Signal peptide:

amino acids 1-32

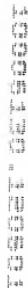


FIGURE 163

GCTGTTCTCGGCCACCACTGGCCGCCGGCCGCAGCTCCAGGTGTCCTAGCCGCCAGC
 CTCGACGCCGCTCCGGGACCCCTGTGCTCTGCGGAAGCCCTGGCCCCGGGGCGGGCAT
 GGGCCAGGGCGCGGGGTGAAGCGCTTCCCAGGGCGTGACTGGCGGGCTTCAGCCAT
GAAGACCCCTCATAGCCCTACTCCGGGCTCTGCGCGCAGCGTCAGGCCAGGCTGACC
 GGAGCCAGCGCTCTACGGAGGACCTCGCCTGCGCGAGGGCTGGGAGATGGGGACT
 GGATCCAGCATCCTCTCCGCCCTCAGGACCTTCTCTGTCACCTGGCTCAATAGTCAA
 GGTGGAAAAGCAGCTACAGGTACAGTCAGTCCAGTGGCTCTGCTTCCTGTACTGG
 GAGTGGCCTGCAGTGCACATCTGTACATATTCTGCACTGATTGCTGGCTCATCGCTGTG
 CTCTACTTCACTGGCTGGTGTGTTGACTGGAACACCCAAGAAAGGTGGCAGGAGGTACA
 GTGGGTCCGAAACTGGGCTGTGGCCTACTTCGAGACTACTTCCCATCCAGCTGGTGA
 AGACACACAACCTGCTGACCACCAGGAACATATCTTGGATACCACCCCATGGTATCATG
 GCCCTGGGTGCCCTCTGCAACTTCAGCACAGAGGCCACAGAAGTGAAGAAGTCCCAGG
 CATACGCCCTAACCTGGCTACACTGGCAGGCAACTCCGAATGCCCTGTGTTGAGGGAGTACC
 TGATGTCGGAGGTATGCCCTGTCAGCCGGACACCATAGACTATTGCTTCAAAGAAT
 GGGAGTGGCAATGCTATCATCATCGTGGTGGGGTGGCGCTGAGTCTTGAGCTCCATGCC
 TGGCAAGAATGCACTGACCTGGCAACCGCAAGGGCTTGTGAAACTGGCCCTGCGTCATG
 GAGCTGACCTGGTCCCCTACTCCTTGGAGAGAATGAACTGTCACAGCAGGTGATCTC
 GAGGGGGCTCTGGGCCGATGGGTCCAGAAGAAGTCCAGAAATACATTGGTTGCC
 ATGCATCTCCATGGTCGAGGCCTTCTCCTCCGACACCTGGGGCTGGTGCCTACTCCA
 AGCCCATCACCACCTGGGGAGAGCCATCACCATCCCAAGCTGGACCCCAACCCAG
 CAAGACATCGACCTGTACACACCATGTAATGGAGGCCCTGGTGAAGCTTCTGACAAGCA
 CAAGACCAAGTCGGCCTCCGGAGACTGAGGTCTGGAGGTGAAC**TGA**GGCCAGCTTCCGG
 GCCAACTCCCTGGAGGAACCAAGCTGCAATCACTTTTGCTCTGAAATTGGAAAGTGTCA
 TGGGTGTCTGGTTATTTAAAGAATTATAACAATTGGCTAACCAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAA

FIGURE 164

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSSGRWGTGSSILSALQDLFSVTWLNR
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIAVLYFTWLVDWNTPKGGRRS
QWVRNWAVWRYFRDYFPPIQLVKTHNLLTRNYIFGYHPHIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLRREYLMGGICPVSRTDIDYLLSKNGSGNAAIIIVVGGAAESLSSM
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA
PCIFHGRLFSSDTWGLVPYSKPITTVVGEPIPKLEHPTQQDIDLYHTMYMEALVKLFDK
HKTGFGLPETEVLEVN

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-
245, 318-323, 378-383

FIGURE 165

GGGCGGCGGGATGGGGCCGGGGCGCGCGGGCGGCACTCGCTGAGGCCCGACGCAGGGCGGGCGGGCG
 GGGCGAGGAGCGCGGGCGGCAAGAGGGCGGCGGGAGGCGACGCCGGGAGCAGGCCGAGCAGCAGGTGGCG
 CGGGCTGCAGGCTTGTCAGGCCGAAGCCCTGAGGCCAGCTGTTCCACTGGCTCTGCTGACCTTGCTGCCCTTGGGA
 CGGCCTGCTCAGCGAGGGGCCGTCACCCGCTCTGAGCACGCCAATGGCCCTGCTGCCCTTCTGAGAGACCCA
 GTTCTGCTGCTGACCTGCTGGTCGGCTTGTCTCTGTTGAGTGGCTCTGGCATCAACTTCTGCTCCAGCTGTCAC
 GCTGGCGCTCTGCCGGCTCAGCAAGCAGCTAACCGCCCTCACTGCCCTGCCCTACTCACTCTGGAGCCA
 ACTGGTCTATGCTGCTGGAGTGGTCTGCAAGCGGAAGTGGAGGAGGACCCGTTGAGGAGCTGAGGCC
 TGGAAAGGAGCACCGAGTCATCATCTCAACACAACTTCAGGATCTGACATTCTCTGTTGGGGACCATGTTGA
 CGCCTTCGAGCTGCTGGGGAGCTCCAAGGTCTCTCTAAGAGGGCTGCTCACTGTCGCCCTCATGCCCTGGAC
 GTGGTACTTCTGGAGATTGTTCTGCAAGCGGAAGTGGAGGAGGACCCGTTGAGGAGCTGAGGCC
 CGCCTGTCGACTACCCCGAGTACATGTTCTCTGACTGCGAGGGAGCCTTCAAGGAGACCAAGCA
 CGCGCTTACGATGGAGGTGGCGCTGCTAAGGGCTTCTGTCCTCAAGTACCACTGTCGCCGGACCAAGGG
 CTTCAACCACCGAGTCAGTCAGTCCTCCGGGGACAGTCGCCAGCTGCTATGATGTAACCCCTGAACCTCAGAGGAAA
 CAAGAACCCCTCCCTGCTGGGGATCCTACGGGAAGAAGTACAGGCCGGACATGTCGCTGAGGAGATTTCTCT
 GGAAGACATCCCGCTGGAGTAAAAAGGAAGCAGCTGAGTGGCTCATAAACTGTCAGGAGAAGGCCCTGCTCCA
 GGAGATATAATACTAGAAAGGCCATTTTCAGGGAGGAGCTTAAGGCTGCCGGAGGGCTGGACCTCTGAA
 CTTCTGTCCTGGGCCACCATCTCTGCTCTCCCTCTGAGTTGTTGCTTGGGGCTTGGAGACTGTCAGACTGATAGGAGAATCGCT
 TCTCTGATCTGACTTCTGGGGTTGTGGAGCAGCTCCCTTGGAGTTCGAGACTGATAGGAGAATCGCT
 TGAACCTGGGGGGTGGAGATTGCATGAGCTGAGATGGCATCACTGTACTCCAGCTAGGCAACAGAGCAAGACT
 CAGTCTCAAAAAAAAAAAACAAAAACCCAGAATTCTGGAGTTGAACTGTGTAGTTACTGACATGAAAA
 ATTCACTAGAGGCTGAACAGCAGATTGAGCAGGAGAAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT
 TTTCAGGCTATGAAAAAGAATGAAGGAAAATAACAGCCTCAGAGACCCATGGTGACCGTACACAAATCAA
 CATATGCTGATGAGGAGTCCCAGAGGGAGGAGGAGGAGGTCAGAAGAATGGCCCAAGACTGATGAAAAAA
 GTAAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGATATCAGAGATCCACACCTAGATTTCT
 ATACAAACTGTCAAATGACAAGAAATCTGAAAGACAGCAAGAGATGACCAACTTATCTGTTCAAGGATCTTG
 ATCAGATTAACAGCTCATTCCTCAGAAATCATGGAGGCCAGGAGATAGTGGGATGAAACACTGTGAAAGGAA
 AACCTTCAACTGTAATTATGGACTTTGAGTCTTAGATGGCTCTGACCTCTTGTCTCAGGGACAGTTTCA
 ATTTAACTCTAATAACAAATTAGTCAGCTTCTGACCTGTAGGAAGGCCGTCTTCTAGGCCGGACAGCTGGC
 TTACACCTGTAATCCAGCAGCTTGGAGGCCAGACGGGTTGAGTCATTGGGGTCAGGCTGATCTCAAACCTCT
 GAGITCAGGCTGATCTGCCGCCCTCAGCTCCTAACAGTGTGATTCAGGCCGTGAGGCCACTGCCCTGGCGGA
 ATTTCTTTAAAGGCTGAATGATGGGGAGGCCAGACGGGCTGATCTCAGGCCGTGATCTGGGATTTGTA
 AACATGACCCACCATGCTGGCTATTTGATTTAGTAGAGAGCTGTTAGCCAGGCTGGTCTGACCTCT
 GACCTCAAGTGAACACCTGCTCAGCTCCCAAAGTACTGGGATTACAGGGCTGAGCCACTGTCCTGCCCTTG
 GCATCTTGATGTCATTGGCAATTGTTATCTCTATCTCTTGGGGAAATGTCGTTCAAGCTCTTG
 CCTTTTAAATTCTTATTATTTATTATTTGAGACAGGGCTTGTCTGTTGCCAGGCTGGAGTA
 CAGTGGCACAGTCCTGGCTACTGCAGCTCGACCTCTGGGCTGAGCTGATCTCCACCTCAGCTCCCTTG
 AGCTGTTATTTTTGATTTGATTTGAGCTGTTGATTTTGATTTTGAGGAGACAGCATTTCACCTGA
 TGCCCAAGGCTGGCTGTAACCTGAGCTCAAGCTGATCTGCTCTGAGCTCCAGGCCCTCCAAAGTGTGGGATTACAGA
 CATGAGCCACTGCACTGCCAAACTCCCCAAATTCAACACACACACACACACACACACACACACACAC
 GAGGGGCCGGGTGTCGCCCAACTACCGGGAGACTGAGGAGGAGATCGCTGGGATGAGAAGTCGAGGCTG
 CAGTGAGTCGAGGTTGTCGCACTGCAATTCCAGCCTGGACACAGAGTGAACCCCTGTC

FIGURE 166

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTKQFVLHLLVGFVVFVSGLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLV
MLLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFIEDFLCGWTMCERFGVGLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCRKWEEDRTVVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKK
YEADMCVRFFPLEDIPLEDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLLN
FLSWATILLSPFSVFLGVFASGSPLLITFLGFVGAASFVGVRRLIGESLEPGRWRQLQ
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTATTTAAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGCA
GCCACCAGGCATATTCACTTTGTGTGTTTCTTTGCTTAGCAGGGCACTGGGCACTTCTT
GCTTATTCTTGGTAGAAAGGGCTCAGTTGTCTTGTTGGGGTGGCAGGCAGGCCG
GCTTACGCCTGATACGGGCTGGGTTAGAAGGGAAAGGAAAGATAAAACTTTATACAAATGGG
GATAGCTGGGTCTGAGACCTGCTTCTCAGTAAAATTCTGGATCGCTATACCTCTT
TTCTCTAACCTGGCATACCCCTGTTAACGGCTCTCACGGCTTCTCTGTTCTAGGATCAA
AGTATTAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCTGGCAGCTTATTGT
ACATGTGGTGTCTTGTCTGCTTGTTAATGTTGATGCCATGGGTGTTGACAAGCC
TTCCTTTGGCTGGACACTGTTCCCTGCCCTCCCTACTCTTCTACTTAATATGTAGTC
ATCCCTGCAGATTCAATTCAACATCATTTCTCCAGGGATCTGGCCTGACAGAACTCAT
CTTGTAAATGCTCTCATAAAGACCACTGTTCCCTTGCAGCAGCTGCCACTCAGTTGTA
TCTTTATGTGCGTTGGTTGTATGGGTTGTCTGCTTCCCCAGAATGCCAGCTGAGC
TGCCTGAGGGTCAAGGGCATTGCTGTGCCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT
CATGTTTAGAGACTAAATGGAGGGAGATGAGGAAAGATTGAAATCTCTCAGTTCACCA
GATGGTGTAGGGCCCAGCATTGTAATTCAACACGTTGACTGTGCTTGTGAATTATCTGGGGA
TGCAGGCTCTGATTCACTGAGGCCAGGTGGCATCTCAACAAACTCCACGTGATGCTGA
TGCTGGTCTATGAACTATACAAATAGTAAGAATCTATGGAGCCAGGCTGGCATGGTGGC
TCACACCTATGATCCCAGCATTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
TCAAGACTAGCCTGGCAACATGGGAAACCCATCTGACTAAAAAATACAAATTAGCTG
GGCATGGTGGCACATGCCCTGAGTCCAGTGAAGCCAGATCAGGCCACTGTATTCAAACCAGGGTGAC
AACCTGGGAGGCGGAGGTTCCAGTGAAGCCAGATCAGGCCACTGTATTCAAACCAGGGTGAC
AGAGTGAGACTCTATGTCCAAAAAAAAAAAAAA

FIGURE 168

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSLQCPGAATRHIHLCVCFSLALGHFLLISLVGKGLSLSGVGGRQAGRLIRPWVRR
EGKINFYTNQDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPEWS
GPPCPGQLHCTCGVLLSFL
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Important features of the protein:

Signal peptide:

amino acids 1-28

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FIGURE 169

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCAAGGTGCTGTGA
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTCAGCAACTAAAAAGCCAC
 AGGAGTTGAACGTCTAGGATTCTGACTATGCCTGTGGTGGCTAGTGCTCTACTCCTACCTAC
 ATTAAAATCTGTTTTGTCTCTGTAACTAGCCTTACCTTCCTAACACAGAGGATCTGT
 CACTGTGGCTCTGCCAACCTGACCTCACTCTGGAACGAGAACAGAGGTTCTACCCAC
 ACCGTCCTCGAAGCCGGGACAGCCTCACCTGCTGGCTCTCGCTGGAGCAGTGCCTC
 ACCAACGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGAGCTGAGGCTTGAACAGCTTGGTA
 GCTCGGCTTCAAGGTGGCCTTGCCCTGGCGTAGAAAGGGATTGACAAGCCCAGAGATT
 CATAGGCGATGGCTCCACTGCCAGGCATCAGCCTTGCTGTAGTCATTCACTGCCCTGGGG
 CCAGGACGGCCGTGGACACCTGCTCAGAACGAGCTGGGTGAGACATCACGCTGCCGCCAT
 CTAACCTTCATGTCCTGCACATCACCTGATCCATGGCTAATCTGAACACTGTCTCCAAGG
 AACCCAGAGCTTGAGTGGAGCTGAGCTGAGCTCAGACCCAGAACGGGCTGCTTAGACCACCTGGTT
 TATGTGACAGGACTTGCATTCTCCTGAAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA
 GGGAAAGGAACCTGTGCAAATTATGGGTAGAAAAGATGGAGGTGTTGGGTTATACAAGGC
 ATCGAGTCTCTGCATTCACTGGACATGTGGGGGAAGGGCTGCCATGGCGCATGACACACT
 CGGGACTCACCTCTGGGGCATCAGACGCCGTTCCGCCCGATCCACGTACCAAGCTGCTG
 AAAGGCAACTCAGGCCATGCTCATCAGCAGGCAGCAGCCAAATCTGCGATCACCAG
 CCAGGGCAGCGTCTGGGAAGGAGCAAGCAAAGTGACCTTCTCCCTCCTCCCTC
 TGAGAGGCCCTCTATGTCCTACTAAAGCCACAGCAAGACATAGCTGACAGGGCTAATG
 GCTCAGTGTGGCCAGGAGGTCAAGCAAGGCTGAGAGCTGATCAGAAGGGCTGCTGTGCG
 AACACGGAAATGCCCTCAGTAAGCACAGGCTGAAAAATCCCCAGGCAAAGGACTGTGTGGCT
 CAATTAAATCATGTTCTAGTAATTGGAGCTGTCCTCAAGACCAAAGGAGCTAGAGCTTGGT
 TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAAATTGAAACCCCAA
 TCCAAACCTAAGAACCGAGGTGCAATTAGAATCAGTTATTGCCGGTGTGGTGGCCTGTAATG
 CCAACATTTGGAGGCCAGGCGGGTAGATCACCTGAGGTCAAGACCAAGCCTG
 GCCAACATGGTAAACCCCTGTCTACTAAAAACAAAAAAACTAGCCAGGCATGGTGGT
 GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
 GAAGGAGGCTGAGACAGGAGAATTCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
 AAAAATAAAAAGAATTATGGTTATTGTAA

FIGURE 170

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRD
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Signal peptide:

amino acids 1-15

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FIGURE 171

GC GG GGG CCG CGAG TCC GAG ACCT GT CC CAG GAG CT CAG CT AC GT GAC CT GT CA CT GC CT C
 CC CG CC GC CT CCT GC CC CG CC **ATG** ACC CAG CC GG GT G C C C C G G C T C T C G T G C C C G C G C T
 GG C C C T G G G C T C A G C C G C A C T G G G C G C C T T C G C C A C T G G C C T C T C C T G G G A G G C G G T
 G C C C C C C A T G G C G A G G C C G C G A G A G C A G T G C C T G C T T C C C C C G A G G A C A G C C G C C T G T G G
 C A G T A T C T T C T G A G C C G C T C C A T G C G G G A G C A C C C G G C T G C G A A G C C T G A G G C T G C T G A C
 C C T G G A G C A G C C C G A G G G G A T T C T A T G A T G A C T G C G A G C A G G C C A G C T C T T G G C C A A C C
 T G G C G C G C T C A T C C A G G C C A A G A A G G C G C T G G A C T T G G C A C C T T C A C G G G C T A C C C G C C
 C T G G C C C T G G C C T G G C G C T G C C C G G A C G G G C G C T G G T G A C C T G C G A G G T G G A C G C G A
 G C C C C C G G A G C T G G G A C G G C C C C T G T G G A G G C A G G C C G A G G C C G G A G C A A A G A T C G A C C T C C
 G G C T G A A G C C C G C T T G G A G A C C C T G G A C G A G C T G C T G G C G G C G G G C G A G G C C G G C A C C T C
 G A C G T G G C C G T G G T G G A T C G G G A C A A G G A A C T G C T C C G C C T A C T A C G A G C G C T G C C T G C A
 G C T G C T G C G A C C C G G A G G C A T C C T C G C C G T C C T C A G A G T C C T G T G G C G C G G G A A G G T G C T G C
 A A C C T C C G A A A G G G G A C G T G G C G G C C G A G T G T G C G C A A A C C T A A A C G A A C G C A T C C G G C G G
 G A C G T C A G G G T C T A C A T C A G C C T C C T G C C C C T G G G C G A T G G A C T C A C C T T G G C C T T C A A G A T
 C **T A G G G C T G G C C C T A T G T G A G T G G G C T C G A G G G A G G G T T G C C T G G G A A C C C C A G G A A T T G A C
 C C T G A G T T T A A A T T C G A A A A T A A A G T G G G C T G G G A C A C A**

FIGURE 172

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQPVPRLSVPAALALGSAALGAAFATGLFLGRRCPWRGRREQCLLPPEDSRLWQYLLSRS
MREHPALRSLRLLTLEQPQGDMMTCEQAQLLANLARLIQAKKALDLGTFGTGYSALALALAL
PADGRVVTCEVDQAPPPELGRLWRQAEAEHKIDLRLKPALETLDDELLAAGEAGTFDVAVVDA
DKENCSAYYERCLQLLRPGGILAVLRLWRGKVVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

FIGURE 173

CCGGCCGCCGAGCCGCTACCCCGCTGAGCCGCTTCCGCCCTGGCCTCTGCCGTCA
 GC**ATG**CCACACGCCCTCAAGCCGGGGATGGTGTTCGCTAAGATGAAGGGCTACCTCAC
 TGGCCTGCCAGGATCGACGACATCGCGATGGCCGCTGAAGCCCCCACCAACAAGTACCC
 CATCTTTCTTGGCACACAGAAACAGCTCTGGACCCAAGGACCTGTCACAGGGCTG
 ACAAAATGTAAGACAAGTACCGGAAGGCCAACAGGAAAGGCTTCAATGAAGGGCTGTGG
 GAGATCCAGAACAAACCCCAACGCCAGCTACAGGCCCTCCGCCAGTGAGCTCCGCACAG
 CGAGGCCGCCAGGCCAACCCGCCAGCCAGCTGACGAGGACATGAGGAGGCCGG
 GGGTCATGCCGTACAGCGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGGACTCA
 GACTCAGAACAGAGTAGCCGACAACAGTGGCCTGAAGGAGGAAGACGCCCTGCCCTAAAGATGTC
 GGTCTCGAAAGCGCCGAAAGGCCCTCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG
 AAAGAGGAAGACTCGGAAAGCTCATCTGAGTCGGAGAAAGACCAAGGCCAGGACTTCACACCT
 GAGAAGAAAGCAGCGGTCTGGCGCCAGGAGGGCCCTCTGGGGGACGGAAAAAAAAGAA
 GGCGCGCTGAGCCGCTCCGACTCCAGCTCAAGGCCGATTCGGACGGGGCAAGGCTGAGCGG
 TGCCCATGCCCGTCTGCCGCTCTCTCTCTCTCTCCGACTCCGACTCCGATGT
 TCTGTGAAGAACGCTCCGAGGGCAGGAAGCCAGCGAGAACGCTCTCCGAAGCCCGAGG
 GCGGAACCGAACGCTGAACGCCCTCCGCTCAGCTCCAGCTGACAGTCAGCCGAGG
 TGGACCGCATCAGTGAGTGAAGCGCCGGGAGCAGGCGGGAGGCCAGAGCTGGAGGCCGG
 CGCGCCGAGAGCAGGAGGAGGAGCTGGCGCGCTGGGGAGCAGGAGAAAGGAGGAAGGA
 GCGGAGGCGCGAGCGGGGCCACCGCGGGAGGCTGAGCGGGCAGCGCGCAGCACCGGG
 ACGACTCAGGGAGGAGCATGAGCCGTCAAGAACGGGGAGCGAACGGGGGGGGGGGG
 CCCCGCTCTCTCTGACTCTCAGGCCGAGGCCAGCTGGAGAGAGGCCAAGAAATCAGC
 GAAGAACGCCGAGCTCTCAAGCACAGAGCCGCCAGGAAACCTGGCAGAAGGAGAGAG
 TGCGGCCGAGGAGAACACAAGCCAAGCCGACGGCTGAAGGTGGAGCGGACCCGGAAGCGTCC
 GAGGGCTTCTCGATGGACAGGAAGGTAGAGAAGAAAGAACGGCTCCGTGGAGGAGAACAGT
 GCAGAACGCTGCACAGTGAGATCAAGTTGCCCTAAAGTCAGCAGCCGGACGTGAAGAGGT
 GCCTGAATGCCCTAGAGGAGCTGGGAACCTCTGAGGTGACCTCTCAGATCTCCAGAAC
 ACAGACGTGGGCCACCTTGAGAGAGATTGCGCTTACAAAGCGAACAGGACGTATGGA
 GAAGGCAGCAGAACAGTCTATAACCGGCTCAAGTCGCGGGCTCTCGGCCAAAGATCGAGGG
 TGCAAGAACAGTGAACAAGGCTGGGATGGAGAAGGAGAACGGCGAGGGAGAACGCTGGC
 GAGCTGGCCGGGGAGGAGGCCCGGAGGAGAACGGGGAGGACAAGGCCAGCACGATCTC
 AGCCCCAGTGAATGGCGAGGCCACATCACAGAACGGGGAGAGCGAGGACAAAGGACACG
 AGGAGGGCTGGGACTCGGAGGAGGGGCCAGGTGTGGCTCTCTGAAGACCTGACGACAGC
 GTACCGGAGGGTCCGACCTGGACAGGCCCTGGAGGCCAGGAGGGCAGGAGGCCAGGGAC
 GGGGACTCGGAGGCCCTGGACAGGAGAGCTGAAGCCGCGGCCAGGCCAGGCCCAGCCCC
 CCGAGCTCAGGCTGCCCTCTCTCCCGGCCAGGAGGAGCAGGAGAGAACACTGTGGG
 GAACCTGTCGTTGCTGTTGATTTGTTCCCTGGGTTTTTTCTGCCATAATTCTGTGATT
 TCCAAACCAACATGAAATGACTATAAACGGTTTTAATGA

FIGURE 174

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNKYPPIFFFGTHTAFLGPKDLPYD
KCKDKYGPKNKRKGFNEGWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDDERG
VMAVTAVTATAASDRMESDSDKSSDNSGLKRKTPALKMSVSKRARKASSLDQASVSPSE
EENSESSSESEKTSQDFTEPEKKAAVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSDSVVKPPGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDEV
DRISEWKRRDEARRRELEARRRREQEEELRRRLREQEKEEKERRERADRGEAERGGGGSGD
ELREDDEPVKKRGRKGRGRGPSSSDSEPEAELEREAKSAKKPQSSTEPARKPGQKEKRV
RPEEKQQAKPVKVERTRKRSEGFSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSVDVKRC
LNAALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAEEVYTRLKSRLGPKIEAV
QKVNKAGMEKEKAEEKLAGELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDKEHE
EGRDSEEGPRCGSSEDLHDSVREGPDLDLPGSDRQERERARGDSEALDEES

Signal peptide:

amino acids 1-13

FIGURE 175

GTGGGTTCTGGATCTTACCAACTGAGATCTGGGACTCATGCCCTAATAATTATTAATTAA
 ACACCATTTGAAAGAGAACATTGTTTCATCATGAATGCTAATAAGATGAAAGACTTAAAGCCAGAACGCAAGA
 TTTCACCTTTCTGTTGATGCTAACGATGCCATTGTTCTTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG
 AAATATCCCAAGACTCAAGCTAACCTAACAAAGACTGCTTCAAAAGTGCTTCAATAGCTGTATTCCCTTTGGGTCATC
 AGAAGGACTGGATTCAAACCTCTCTTAGATGAGGAAAGAGGCAGGCTGCTCTGGAGGCCAAAGAACACAT
 CTTCTACTCAGTGGTTGACTTAAACAAAATTAAAGAAGATTATGGGCTGCTGCCAAAGGAGCGGTGA
 ATTATGTAATTTAGCTGGGAAAGATGCCAACTGGCAATTCTCATGAGACTTCAAGACTCTAGCCCTATAACAA
 AACTCACATATATGTGTGAACTGGGATTCATCCAAATATGGGTATATTGATCTGGAGTCATCAAGGA
 GGATATTATACAAACTAGACAGGAAACACAAATTGGAGTCTGGCAGACTAAATGCTTCTGATCCCTCAGCAGCC
 TTGGCTCATGATGACAGATGACTCTACTGGAAACAGCTCTGATTTCTGCCAAAGATACTGCAATT
 CACTCGATCCCTGGGCTACTCATGCCAACACTACATCAGAACCTGACATTTCAGAGCACTACTGGCTCAATGG
 AGCAAAATTGGGAAACTTGGAACTTCTGGGATCATCAGACACCCTACATCAGATGATGATAAAATTCTCTTCTTGG
 TGATCATCTCAAGAACGCACTACCTCCGATAAAACCATCTTCTGGTCAAGGAGAGTTGTAAGAATGATGT
 AGGAGGACAACGGCAGCTGATAACAAACTAGGTCAGCTTCTGGGAGACTGTTTCTCAATTCTGGAG
 TGATGGGCAAGATACCTTTGAGCTTCAAGATAATTATTACTCCCAAAGAGATGAAAGAAATCTGT
 AGTATATGGGATCTTCAACTAACACGGCTTCACTTCAAGGCTCTGCTGTTGTGTGATAGCATGGCTGACAT
 CAGAGCAGTTTAACTGGCTCATAGCTCATAGGAAAGTCCAGACCACTGGTGGGTCAGTATGATGGGAGAA
 TCCCTATCCAGGCTGGTACATGTCAGCAAACCTATGACCACTGATTAAGTCACCCGAGATTCTCAGA
 TGATGATCATGTTTCTGGAACTTCAAGACACTCTGGTGTGAGTGGGAGACTGTTCTCAATTCTGGAG
 TGTAATGTTTCTGGGAAACAGACATTGGAACTCTCTCAAAGTGTGAGCATTTCAGGAAAGATGGAAATATGG
 AGAGGTAGTGTGGAGGGAGTGGAGATCTTCAAGACTCATTCAGATCATCTGGAAACATGGGATTTGCT
 GCAACAAATTGTATGATTGGTCTCCGAGATGGATTAGTCACTGCTCTGGCAGATGCGACACTATGGGAAAGC
 TTGGCAGAGACTGTGCTGGAGGCCACTCTGGCTGGTGGGATGAAATGCAAGCTCTGGATATGCTTCTAC
 TTCTAAAGAGGAGCTAGACCCGAAAGTCAAAATGTCAGGCCAACTACCCAGTCTGGGACATCGAACAG
 CATTAGTCAGAACATGCTGATGAAAAGGTGATTGGCATTTGAACTTAACTCAACCTTCTGGGATGTATACC
 TAAATCCCAACAGCAATTAAATGGTATATCCAGGGTACTGGGATGAGGATGGGAGGTTGAGCCG
 TGAAGAATCATCAAAAGGAAATTGGGCTACTGTCAGGTTGAGAGGATTCTGGGATGTATTACTG
 CAAAGGCCCCAGGACACACTTCTGGCAGACCATGGTGAAGCTGGATTGAAATGCAAGACAGTGG
 AAATACCCAGGAGGCCAGCATGGTGAAGGGGGCAGGGTCAAGGATCTTGGGATGAGTCAACAAAGA
 CTACATCCTAACTTCTGGCAGACCCAAACTTCTGGCTGCCAACCTACTGGCAGGCCACTGCGAACAG
 GAGACAGAAAACAGGGGGCCCAAAAGTGGAGGACATGCGAGGAAAGAACAAATCGAGAACATCA
 CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCAGCTAGTTTCTACTTAAATTAAAGAAAATTCCTTAC
 TATAAAACATGGGTTAAATTAGTGTATATCTGGATTTAGTAACTCATAAAATGCTTCCCATGGGATTGCT
 TGAAGAATCATCAAAAGGAAATTAAGGAACTTCTGGGATGAGGAAAGGGGAAATTCTTCAAGGAGCTT
 CCAAGAACAAATTCTGGCACAACAAAGTATAAGGAAATCTGGGATGAGGAAATGCAATGTAATGTTT
 GTTTTGAGTTTGGAAATTATGTCAGTAAATTGAGCTGAGCTAACGCCCCGAAATTGATGAGTCTATAGG
 GCCTTATCCCTGGAATGCTCATTAAGCATGGAAATTACCATGCACTTGTGCTATGTTCTTATGAAACAGATATA
 CAATTCTATGAGAACAGCAGCTACCTTGTGAGGGAAATAGAGGCTCAGACACAAATTAAAGCACACTCCATTATC
 AACAGAACATTCTCAGTGGACCAITCACTCTGGGAAATGGTATAGGAATTGGGAGGGTGCATTATTCTTCTC
 TGGGACTCTTCACTAGGGTATAAGTACTGCTCAATTGTAATTCATCTGGTAAAAAATCTAGATTATAACAA
 ATTGACTAGTCAGGAGTAACAGGTTCAAGAGAGGTTGGTCTCTAGTTATGTTTCTAGGATATACTAA
 GCCTCACAGGGACAGAAATGCTTAATAAACTTTAATGAGATGGGAAATATTAAATAAAACAGGAAACAC
 TAATGATTTAATGCTCATGGGAAGGCCATGCGAGTGGGATTTGTTAGAGAACAGAGGAAAGAACGCCAT
 AAATTCTGGCTTGGGAAAACATCATACCCCATGAAAGAACAACTCACAAATAAGTGAGGAGTAATGAA
 TGGAGCTCTTCACTAGGGTATAAGTACTGCTCAATTGTAATTCATCTGGTAAAAAATCTAGATTATAACAA
 AACTGCTAGAACAAATCTGGGAAACATAAAATTCTCTGGGAACTAGGAGTACAGGATTTTATTAACCC
 AAATGATTTCTGGTATATTGGGTTTGTGATTATATTGAGTGAATAGGAGGAAACAAATATAACACACAGA
 GAATTAAGAAAATGACATTCTGGGAGTGGGATATATTTGTTGAATACAGAACGAGCTAAATTAA
 AACGGAAAGGGTTAAATTAACTCTTGTGACATCTCACTCAACCTTCTCATTGCTGAGGTTAATCTGTTAATT
 GTAGTATTGTTTGTAAATTAAACAAATAAGCCTGCTACAT

FIGURE 176

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTKQNIPLRKLTYKDLLLNSNCIPFL
GSSEGLDFQTLLLDEERGRLLLGAKDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLSSGTASDFLGKDTAFTRSLSGPTHDDHYIRTDISEHYWLNGAKFIGTFF
IPDTYNPDDDKIYFFFRESSQEGSTSADKTIILSRVGRVCKNDVGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVYGVFTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDPDVISFIKRHSVMYKSVYPV
AGGPTFKRINVVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSIISKEKWVNMEEVVLEE
LQIFKHSSIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCLARDPYCAWDGNA
CSRYAPTSKRRARRQDVKYGDPITQCWDIEDSISHETADEKVIFGIEFNSTFLECIPKSQQA
TIKWIYQRSGDDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYYCKAQEHTFIHTIVKLTLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPWKHMQMEEKKRNRHHRDDELPRAVAT
```

Important features of the protein:

Signal peptide:

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCTGACCTCCCTGAGGCCAACACTGAGCTGGAGGCCAGGGTCATCCTGGAGCATGCCACCAGGGGGAGCAGA
 CAACCTCCCAGGTAAAGCTGGGAGCAAGCTGAAGCTGTGTTCTCAGGAGCTGGTGTATTCCCCACCCAC
 CTCAAGCTTCAAGCCAGGGACTGATCAAGTTGTGTCCTGGAGTGGGGAGCAGAAGGGCTGGCTGGCAAGA
 GTGGCCCTGGAGAAAAGAGGTTCAAGCCTTGACCGCCGAGCTGGCCCTGACTAAAGATCAGAACCCATGGGCATC
 GGGTGAGGTGGGGGGCACAGGTGTATGTCACCTCTCTGTCTCAAGAAGAGCTGAGAGAGGGATCTTG
 AGCCATTGAGGTCTATGGAGCTACAGAGGGAGGAAAGGTATTTAAGGTAAACAGTGTGGCACAAATGTTAA
 GAGCACAGTGGCTTCAACCTCTTGGACTCAATTCATCACTAAAGTAGGGCCAAATAATGACACCCACTCAT
 AAGGGACTGACTTAACCTCTTGGACTCAATTCATCACTAAAGTAGGGCCAAATAATGACACCCACTCAT
 AAGGGAGGATTAATGACATAATGTTGATGT**CAT**CACTAAAGTAGGGCCAACTTCAAGTGTGGCCACAG
 TATTTCCACCCACCCCTTCTCTGGCTTCCCAACAGGTACTCAGAACACTGGAGCAGGGCCAGCAGGCTT
 CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTACAGGAAGTGGAGAGACATCCGGCCGGCACAGGTGAGCC
 AGGTGAAGGGGGCTGGCCGGCTGGCCCTGCTGAGGGGGCTGAGCTTCAAGTGTGGAGGGCTGCTGAGCC
 TGACCCAGGGCCAGGATGAGGGGGAGCAGGAGCCGGCTCATGGAGCTGGCCCTCTCAGGAGCTGGCT
 CAAGGGCTGTGGAGATCTGAGGGCTGAGCTTCAAGGAGATGTGAGGAGACAGTCTTGGAGGAGCTCC
 CCCAAGGGCTGGAGGAGGCCCCCTCCCTGGCTCAGACAGTGGTATTCTGCTATCAGGAGGGCTGGAGGATG
 AGGTGACAATCACGGAGGTAGTGCTGTGGAGGTATGAGGGAGATGCTGAGGAATGGGTCAAGGCTCGGA
 ACCAGCAGGGCAGGGTAGGTGGCTTGTGCTTCAAGGAGATATCTCAGTCCCGGGACCTCTCCCTCC
 AAAGACAGTGAACATCCTCCGGGGCAGGCCCCACAGCATCTCTGGCAACAGGCCCTGTACAGCTACAC
 GTGCAAGGGAGCTGAGCTTCTCTGGGGGGCATCATCTGGCTGTGGCCGGGGCCAAAGATGGAGTATGAGC
 GCTTCTGGAGGGAGAAATTGGGGGGCTGTGGGGCTCTCTCTCTCTCTCTCTCTCTCTCT
 CAGGGCACCTGTAACCTCTGACCTGAGCATCTGGCTGTGGCTGGGGGACAAAGCTGGGACTCTGGGGTCTGG
 CTACCTCTGTGGAGATGGGGGGCTCTGGGGGACACTCTGGGGGACTCTGGGGGGGGGGGGGGGGGGGGGG
 ACATGATGGCACCTCGACTCACGGGGATGCTGTCACCCACCCCCGGGGCTAAACCCCCGGATCTGGGG
 CAGATCCCCCTAC**TGA**AGGGAGGAGGGGGCTGACCCACTGTGGCTGTGGCTCTCTCTCTCTCT
 CGAACACATCAATGATCAGACAGAACACAGGAAAGCTGGAACTCCGGCTTATTTCCACCTCACCT
 GGAAACTCTGCCCCCTCCCATTTCTAGAGCTGGAAACCCACTCTCTCTCTCTCTCTCTCT
 GGAAACTACTCTGCT
 ATCCATCAAGGTCTCTAGTTCTGGGACCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
 CCAGGGGACTCTGGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
 CTGTAATGGTGTGGCAGGATTCTGACATGAATAAGGGCAGCAGGGCAGGGCAGGGCTGGGGGGGGGG
 CTAAGAGGGGGAGGGGGCTTCAAGGCTGTGGCTTGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
 GCTCTATCATGGAGGGTGTGGGGAGGG
 TGAGGGGGCTGTGACCTCTCTGG
 AGCTGG
 TCCATCACACATGAGGGAGGAGCTGG
 TTTTCCCCCTGGGGGGCTCAGGG
 AGTTTACTCTGG
 TTTAGGGCTCAGGCAGACTCACCATACTCCCTGCTCCCTGTGGTAGAGAACACTGAGAGAAC
 TCAACATGAGGGAGGG
 AGTCCCCGGCTGTGTTCTCTACTCTGTGATCAGAGTGTCTGGTTCTGGCTGGCCATTGCTCTGAGTGG
 GCGGGCTGG
 CACAGGGGGTTAGGCTGTCTCTGAGGG
 TCTCAGGG
 GGTCTCTGG
 TCTCAATGTGTGTGACCCGGGAACCTGG
 GCCCTCCCTCTGAGGG
 AGATTTGG
 TTGGGGATCAGGG
 CAGAGAACACAGTGGTCT
 GCCTCTCTGG
 CGTCTCTGG
 TCTATGTTTGTGTTCTACGTTCTTCAAGGATGCTCTTAAACCCCCAGAAGCCCCAATTCTCCCAAG
 TTTCTCTGCTTTATCTAATAAACCTAACATATTAAAG

FIGURE 178

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCPLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPATAEDAEWS
DFEECEETGELFEEPAPQALATRALPCPAHVVFRYQAGREDELTITEGEWLEVIEEGDADEW
VKARNQHGEVGFGVPERYLNFPDLSLPESSQDSNPGCAEPTAFLAQALYSYTGQSAAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRGVFPSSLVEELLGPPGPPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPAAKAPDPGHPDPLT

FIGURE 179A

FIGURE 179B

ATGTGGTGCACTTCACTTCAGTGTCTGAGCATTAGATTTCTCATTTGCCAATAATAACCTCCCTTAGAAG
TTTGTGTGAGATTAATGTAATAAATGAACTCATCCAAACTCTAAAAA
AAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA
AAAAAAAAAAAAGGGAA

FIGURE 180

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLASLPSARLASPLPREEEIV
 FPEKLNGSVLPGSGAPARLLCRLQAFGETILLELEQDSCVQVEGLTVQYLGQAPELLGGAEP
 GTYLTGTINGDPESVASLHWDDGALLGVLYRGAEHLHQPLEGGTPNSAGGPGAHILRRKSP
 ASQGPVCNVKAPLGSPPRRAKRFASLSRFVETLTVADDKMAAFHGAGLKRYLLTVMAA
 AAKAFKHPISRNPVSLVVTRVLIGSGEEGPQVGPSAAQTLRSFCAWQRGLNTPEDSGPDHF
 DTAIALFTFRQDLCVGSTCDLGMADVGTVCDPARSCAIVEDDGLQSFTAHELGHVFNLH
 NSKPCISLNGLPLSTSRLHMAPVMAHVDPEEPWSPSCSARFITDFLDNGYGHCLLDKPEAPLHL
 PVTFPGKDYDADRCQCQLTFGPDSRHCPCQLPPPACAALWCSGHLNCHAMCQTKHSPWDADGTCG
 PAQACMGRCLHMDQJLQDFNIPQAGGWGPWGDCSRTC CGGGVQFSSRDCTRVPVRNGKY
 CEGRRTRFRSCNTEDCPTGSDTFREEQCAYNHRTDLFKSFPGPMDWVPRYTGVAPQDQCK
 LTCQARALGYYVLEPRVVDGTPCSPDSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
 SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQQGNGPHRSIYLALKLPDGSYALNGEYTL
 MPSPTDVVLPGAVSLRYSGATAASETLSGHPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
 PSTPRPTPQDWLHRRAQILEILRRRPWAGRK

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
 172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
 582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGCTCTCAGCCTCTAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**
CAAAGAATCCTCCAGAGAATTGTGAAGACTGTACATTCTAAATGCAGAAGCTTTAAATCC
AAGAAAAATATGTAAATCACTTAAGATTGTGGACTGGTGTGGTATCCTGGCCCTAACTCT
AATTGTCCTGTTTGGGGAGCAAGCACCTCTGGCCGGAGGTACCCAAAAAGCCTATGACA
TGGAGCACACTTCTACAGCAATGGAGAGAAGAAGAGATTACATGGAAATTGATCCTGTG
ACCAGAACAGAATATTCAAGCGGAATGGCACTGATGAAACATGGAAGTGCACGACTT
TAAAAACGGATAACTGGCATCTACTTGTGGGTCTC AAAAATGTTTATCAAACACTCAGA
TTAAAGTATTCTGAATTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
ACAACCTTCTTGAAACAGTCAGTGAATTGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
TTTCTTAAAAATTCAAATTCTGGAGATTGTGATAACGTGACCATGTATTGGATCAATC
CCACTCTAATATCAGTTCTGAGTTACAAGACTTGGAGGAGGGAGAAGATCTCACTTT
CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAAGT
AGAGAACCGCGTCAGCCAGACAAGCAAGTGAGGAAGAACTCCAATAATGACTATACTG
AAAATGGAATAGAATTGATCCCAGTGTGGATGAGAGAGGTTATTGTTGTTACTGCCGT
CGAGGCAACCGCTATTGCCGCCGCTGTGAACCTTACTAGGCTACTACCCATATCCATA
CTGCTACCAAGGAGGACGAGTCATCTGTGTGTATCATGCCCTGTAACTGGTGGGTGGCC
GCATGCTGGGGAGGGTC**TAA**ATTAGGAGGTTGAGCTAAATGCTTAAACTGCTGGCAACATAT
AATAAAATGCATGCTATTCAATGAATTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT
CTCCAGAATTACTGTAGGTAATTCTCTCTCATGTTCTAATAAAACTCTACATTATCACC
AAAAAAAAAAAAAAAAAA

FIGURE 182

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKKAY
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKT
QIKVIEPFSEPEEEIDNEEITTTFFEQSVIWWPAEKPIENRDFLKNSKILEICDNVTMYWI
NPPLISVSELQDFEEEGLHFPANEKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPMMLDERGYCCIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWV
ARMLGRV
```

Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCGGAACCTGGCTCCGGCTGGCACCTGAGGAGCGGCGTACCCCGAGGGCCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCCGACCA**ATGG**CAGCACGGCCGTGCAGCTCTGGGCTTCCT
 GCTCAGCTTCCGGCATGGTGGCACGGTGTGATCACCCACATCCTCACGGCCGTCTACCTGAAAGGGCTGAG
 CAGCGCACGTGGCACCAACATCCTCACGGCCGTCTACCTGAAAGGGCTGAG
 TGTGTGTGGCACAGCACAGGCATCTACCAAGTGCCAGATCTACCGATCCCTGTCGGCGCTGCC
 CCAAGACCTCCAGGCTGCCCGGCCCTCATGGTATCCTCGCTGCTCTCGGCATAGCCT
 GCGCTGCGCGTCATGGGATGAAGTGACCGCCTGCGCCAAGGGCACACCCGCAAGACC
 ACCTTGCCATCCTCGGGCACCCCTCTCATCCTGGCCGCTCTGTGCATGGTGGCGT
 CTCCTGGACCACCAACGACGTGGTGAGAACCTCTACAAACCCGCTGCTGCCAGGGCATGA
 AGTTTGAGATTGGCCAGGGCTGTACCTGGCTCATCTCCTCGCCCTCGCTCATGGT
 GGCACCCCTGCTTGGCTGTCTGCCAGGACGAGGCACCCCTACAGGCCCTACAGGCCCTACAGGCCCT
 CAGGGCCACACGACCACGTCAAACACCGCACCTGCCCTACAGGCCACAGCTGCCCTACAAAG
 ACAATGGGGCCCCCTCAGTGACCTCGGCCACGCACAGGGGTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCTGCTCTCCCTGGCTGCTGGGCTGGGTCCCCGGGGACTGTC
 AATGGAGGCAGGGGTTCCAGCACAAAGTTACTCTGGCAATTGGTATCCAAGGAAAATA
 ATGTGAATGGCAGGAAATGTCTTAGACGACAGGGACAGGGGGAAATAAGAGGAGGAGAA
 AGCTCTATACCAAAAGACTGAAAAAAAAAATCTGCTGTGTTTGATTTATTATATATAT
 TTATGTGGGTGATTCAGGAATAACACAGTTAATATAAAGTGACTTGGAGTTGGTCAGTGGGT
 TGGTTGTGATCCAGGAATAACCTTGCGGATGTGGCTGTTATGAAAAA

FIGURE 184

MASTAVQLLGFLLSFLGMVGTLLTILPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
QCQIYRSLLALPQDLQAARALMVISCLSGIACACAVIGMKCTRCAKTPAKTTFAILGGTL
FILAGLLCMVAWSWTNDVVQNFYNPPLPSGMKFEIGQALYLGFISSSLSLIGGTLCLSCQ
DEAPYRPYQAPPRTTTANTAPAYQPPAAYKDNRAPSVTSAHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

FIGURE 185

GAGCTCCCTCAGGAGCGCGTTAGCTTCACACCCTCGCAGCAGGAGGGCGGCAGCTTCTCG
 CAGGCGGAGGGCGGGCGGCCAGGATCATGTCACCAACATGCCAAGTGGTGGCGTTCCCT
 CCTGTCCATCCTGGGGCTGGCGGCTGCATCGCGCACCGGGATGGACATGTGGAGCACCC
 AGGACCTGTACGACAACCCCGTCACCTCGTGTTCAGTACGAAGGGCTCTGGAGGAGCTGC
 GTGAGGCAGAGTTCAGGCTTACCGAATGCAGGCCATTTCACCATCCTGGACTTCAGC
 CATGCTCAGGCACTGCGAGCCCTGATGATCGTAGGCATCGTCTGGTGCCATTGGCTCC
 TGGTATCCATCTTGCCCTGAAATGCATCCGATTGGCAGCATGGAGGACTCTGCCAAAGCC
 AACATGACACTGACCTCCGGATCATGTTCATTGTCAGGTCTTGCAATTGCTGGAGT
 GTCTGTGTTGCCAACATGCTGGTGACTIONTCTGGATGTCACAGCTAACATGTACACCG
 GCATGGTGGGATGGTGCAGACTGTTAGCAGACCAGGTACACATTGGTGCAGCTGTTCTG
 GGCTGGTCGCTGGAGGCCACACTAATTGGGGTGTGATGATGTCATGCCCTGCCGGGG
 CCTGGCACCAAGAAACCAACTACAAGCCGTTCTATCATGCCCTCAGGCCACAGTGTG
 CCTACAAGCCTGGAGGCTTAAGGCCAGCACTGGCTTGGGTCAACACAAAAAACAGAAG
 ATATACGATGGAGGTGCCGCACAGAGGACGAGGTACAATCTTATCCTCCAAGCACGACTA
 TGTG**TAAT**GCTCTAACGACTCTCAGCACGGCGGAAGAAACTCCCGAGAGCTACCCAAAA
 AACAGGAGATCCCCTAGATTCTCTGCTTTGACTCACAGCTGGAGTTAGAAAAGC
 CTCGATTTCATTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTGTCTCTAAATTCC
 ACCATAAAACAGCTGAGTTATTGAAATTAGAGGCTATAGTCACATTCAATCTCTAT
 TTCTTTTTAAATATAACTTCTACTCTGATGAGAGAATGTGGTTAACTCTCTCTCAC
 ATTGATGATTAGACAGACTCCCCCTTCTCTAGTCATAAACCCATTGATGATCTA
 TTTCCCAGCTTATCCCAAAGAAAATTGAAAGGAAAGAGTAGACCCAAAGATGTTATT
 CTGCTGTTGAATTGCTCCCCACCCCAACTGGCTAGTAATAAACACTTACTGAAGAA
 GAAGCAATAAGAGAAAGATATTGTAATCTCCAGGCCATGATCTCGGTTCTACACTG
 TGATCTTAAAGTTACCAAACCAAAGTCATTTCAGTTGAGGCAACCAAACCTTCTACTG
 CTGTTGACATCTCTTATTACAGCAACCCATTCTAGGAGTTCTGAGCTCTCCACTGGAG
 TCCTCTTCTGCGGGCTCAGAAATTGCTCTAGATGAATGAGAAAATTATTTTTTAAT
 TTAAGCTCTAAATATAGTTAAATAAATATGTTAGTAAATGATAACTATCTGTGA
 AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTGACATTGCT
 ATATGGTACTTGTAAAGTCATGCTTAAGTACAATTCCATGAAAAGCTCACACCTGTAATC
 CTAGCACTTGGGAGGCTGAGGAGGAAGGATCACTTGAGGCCAGAAGTTCGAGACTAGCCTG
 GGCAACATGGAGAAGGCCCTGCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCAGGTG
 GCATACACCTGTAGTCCCGACATTCCGGGAGGCTGAGGTGGAGGATCAATTGAGGCCAGGG
 AGGTTGGGGCTGAGTGCAGTGCAGGCCATGATCACACCAACTGCACTCCAGCCAGGTGACATAGCAGA
 TCTCTGCTAAAAAAATAAATGAAACACAGCAAGTCCTAGGAAGTAGGTTAAA
 ACTAATTCTTAA

FIGURE 186

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSIM
FIVSGLCAIAGVSVPANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHHSVAYKPGGFCASTGFGSNTKNKKIYDGGARTE
DEVQSYPSPKHDYV
```

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAAACTTTCTTCTGTGGCACAGAGAACCTGCTCAAAGCAGAAGTAGCAGTTCCG
 GAGTCAGCTGGCTAAACATCCCAGAGGATA**ATGGCAACCCATGCCTAGAAATCGTG**
 GGCTTCTTGGTGGATGGGGCACAGGGCTGTCACTGTCATGCCAGTGG
 AGAGTGTGGCCTTCATTGAAAACAACATCGTGGTTTGAACCTCTGGAAAGGACTGTG
 GATGAATTGCGTGAGGCAAGGCTAACATCAGGATGCAGTCAAAATCTATGATTCCCTGCTGG
 CTCTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGCTGCTCCGTGATGCTTC
 TTGGCTTCATGATGGCATCCTGGCATGAAAATGCACCAGGTGACGGGGACATGAGAA
 GGTGAAGGCTCACATTGCTGACGGCTGAAATCATCTCATCACGGGATGGTGGTGC
 TCATCCTGTGAGCTGGGTGCAATGCCATCATCAGAGATTCTATAACTCAATAGTGAAT
 GTTGCCAAAAGCTGAGCTGGAGAAGCTCTACTTAGGATGGACACGGACTGGTCT
 GATTGTTGGAGGAGCTGTTCTGCTGCGTTTGTGCAACGAAAGAGCAGTAGCTACA
 GATACTCGATACCTCCATCGCACAAACCCAAAAAGTTATCACACCGGAAAGAAGTCACCG
 AGCGTCTACTCCAGAAGTCAGTATGTG**TAGTTGTGATGTTTTAACTTTACTATAAGC**
 CATGCAAATGACAAAATCTATATTACTTCTCAAATGGACCCCAAAGAAACTTGATT
 CTGTTCTTAACTGCCTAATCTAATTACAGGAACGTGTCATCAGCTATTATGATTCTATAA
 GCTATTCAGCAGAATGAGATATTAAACCCAATGCTTGATTGTTCTAGAAAGTATAGTAAT
 TTGTTTCTAAGGTGGTCAAGCATCTACTTTTATCATTACTCAGATGACATTGCT
 AAAGACTGCATTATTTACTGTAACTTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTAACATTATATCTCACATAGAGACATGCTTATATGGTTTATTAAATGAAATGCCAG
 TCCATTACACTGAATAATAGAACTCAACTATTGCTTCAGGGAAATCATGGATAGGGTG
 AAGAAGTTACTATTAAATTGTTAAAACAGCTTAGGGATTAATGCTCATTATAATGA
 AGATTAATGAAAGGCTTAACTCAGCATTGTAAAGGAAATTGAAATGGCTTCTGATATGCTG
 TTTTTAGCCTAGGAGTTAGAAATCTAACTTCTTATCCTCTCCAGAGGCTTTTT
 TTCTTGTTATTAAATTAAACATTTAAAACGCAGATATTGTCAGGGCTTGCATTCA
 AACTGCTTCCAGGGCTACTCAGAAGAAGATAAAAGTGTGATCTAAGAAAAGTGTG
 GTTTTAGGAAAGTAAATTTGTTTGTATTGAAAGAAGATGATGCTTGTGACAA
 GAAATCATATATGTATGGATATTAAATAAGTATTGAGTACAGACTTTGAGGTTCTC
 AATATAAAATAAAAGAGCAGAAAATGTCTGGTTCTATTGCTTACCAAAAAAAACA
 ACAAAAAAGTTGCTTGTGAAACTCACCTGCTCTATGTGGGACCTGAGTCAAAATG
 TCATTCTGTTCTGTGAAAATAAATTCCTTCTGCTTACCTTGTGTTAGTTTACTAAA
 ATCTGAAATACTGTATTCTGTTATTCAAAATTGATGAAACTGACAATCCAATTG
 AAGTTGTTGTCAGCTGTCTAGCTTAAATGAATGTGTTCTATTGCTTATACATTATA
 TTAATAAAATTGTACATTCTAATT

FIGURE 188

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSIFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYRSQYV
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TCGCC**ATGGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCCCTGACACTGCTGGGCTGGGTG**
 AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTCATCGGCAACAGCAT
 CGTGGTGGCCAGGTGGTGTGGAGGGCTGTGGATGCTCTGCGTGGTGCAGACCACGGCC
 AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCCTGCCACAGGACCTGCAGGCTGCACGT
 GCCCTCTGTGTCATGCCCTCCTGTGCCCTGTCGGTGTGGTCTACCTGCTGGGC
 CAAGTGACCCACTGTGGAGGAGAAGGATTCCAAGGCCGCCCTGGTGTGCTACCTCTGGGA
 TTGTCCTTGTCATCTCAGGGTCTGACGCTAATCCCGTGTGCTGGACGGCCATGCCATC
 ATCCGGGACTTCTATAACCCCCCTGGTGGCTGAGGCCAAAAGCGGGAGCTGGGGCCTCCCT
 CTACTTGGGCTGGCGGCCCTAGGCCCTTGTGCTGGGTGGGGTTGCTGTGCACTT
 GCCCCTGGGGGGTCCAGGCCAGCATTACATGGCCCGTACTCAACATCTGCCCT
 GCCATCTCTCGGGGGCCCTCTGAGTACCCATCCAAGAATTACGTC**TGA**CGTGGAGGGAAATG
 GGGGCTCCGCTGGCCTAGGCCATCCAAGCAGTGGCAGTGCCAACAGCTTGGGATGGGTT
 CGTACCTTTGTTCTGCCTCTGCTATTTTCTTGACTGAGGATATTTAAAATTCTATT
 GAAAATGAGCCAAGGTGGTGAUTCACTCTCACTTAGGCTCTGCTGTTCTCACCTGG
 ATGATGGAGCCAAGAGGGGATGCTTGAGATTCTGGATCTGACATGCCATCTAGAACG
 CAGTCAGCTATGAACTAATCGGGAGGCTGCTTGTGCTGGTTGCAACAAGACAGAC
 TGTCCCCAAGAGTCTGCTGCTGGGGCTGGGCTCCCTAGATGTCACTGGACAGCTG
 CCCCCCATCTACTCAGGTCTGGAGCTCTCTTCAACCCCTGGAAAAAACAAATCATCTG
 TTAACAAAGGACTGCCACCTCGGAACCTCTGACCTCTGTTCTCCGTCTGATAAGACG
 TCCACCCCCCAGGGCCAGGTCCAGCTATGTAGACCCCCGCCACCTCCAACACTGCACC
 CTTCTGCCCTGCCCTCGTCTCACCCCTTACACTCACATTATCAAATAAGCATG
 TTTGTTAGTGCA

FIGURE 190

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWNVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLLALPQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTS
FVISGVLTILIPVCWTAAIIIRDYNPLVAEAQKRELGASLYLGWAASGLLLGGGLCCTCP
SGGSQGPSPHYMARYSTSAPAISRGPSEYPTKNYV

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

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FIGURE 191

GCCAAGGAGAACATCATCAAAGACTCTAGACTCAAAGGCTTCCACGTTACATCTG
 AGCATCTTCTACCCTCGAATTGAACCAGTCTTCAAAGTAAAGGCATGGCATTATCCC
 TTGCAAATTGCTGGCTGGTTCTGGGTCCTTGGCATGGTGGGACTCTTGCCACAACCC
 TCTGCCTCAGTGGTGGAGTATCAGCTTTGTTGGCAGCAACATTATTGTCTTGAGAGGCTC
 TGGGAAGGGCTCTGG**ATG**AATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
 TAGCTCCTTGTGGCTCCCGCTGCCCTGGAAACAGCCCCGGGCCCTCATGTGTGTGGCTG
 TTGCTCTCCTTGATGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA
 GGCTCTAACGAGAGGGCCAAGCATACTTCTGGAACTTCAGGAGTCCTCATCCTGAC
 GGGTATCTCGTTCTGATTCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTCTACA
 ACCCAGCCATCCACATAGGTCAAGAACAGAGAGCTGGAGCAGCACTTTCTGGCTGGCA
 AGCGCTGCTGCTCTTCATTGGAGGGGCTGCTTTGTGGATTTGCTGCTGCAACAGAAA
 GAAGCAAGGGTACAGATATCCAGTGCTGGCTACCGTGTGCCACACAGATAAGCGAAGAA
 ATACGACAATGCTTAGTAAGACCTCCACCGATTATGCT**TAAT**GCTCTCTTGGCTCCAAGT
 ATGGACTATGGTCAATGTTTTATAAAAGTCTGCTAGAAAAGTGTAAAGTATGTGAGGCAGGA
 GAACTTGCTTATGCTAGATTTACATTGATACGAAAGTTCAATTGTTACTGGTGGTAGG
 AATGAAAATGACTTACTTGGACATTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG
 GACCCAATCGCTGCTCCAATTTCATATTCTAAATTCAAGTATACCCATAATCATAGCAAG
 TGTACAATGATGGACTACTTATTACTTTGACCATCATGTATTATCTGATAAGAATCTAAA
 GTTGAATTGATATTCTATAACAATAAACATACCTATTCTA

FIGURE 192

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737  
><subunit 1 of 1, 173 aa, 1 stop  
><MW: 18938, pI: 9.99, NX(S/T): 1  
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER  
AKAYLLGTSGVLFILTGFVLIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL  
FIGGGLLCGFCCCNRKKQGYRPVPGYRVPHTDKRRNTTMSKTSTSIV
```

Important features of the protein:

Transmembrane domains:

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

FIGURE 193

AGT GACA ATCT CAG AGC AGCT CTAC ACCAC AGCC ATT CCAGC **AT** GAAG ATCA TG GGG GT
CTC CCT TCG CTG TGT ACAG TGG CT ATT CTG TAG CAG CT CAG AAG CTG CT AGT CTG CT CC
A A A A A A G T G G A C T G C A G C A T T C A A G A A G T A T C C A G T G G C C A T C C C T G C C C C A T C A
C A T A C C T A C C A G T T G G T C T G A C T A C A T C A C C T A T G G G A A T G A A T G T C A C T T G T G T A C C
G A G A G C T G A A A A G T A A T G G A A G A G T T C A G T T T C T C A C G A T G G A A G T G C **TAA** A T T C C A
T G G A C A T A G A G A G A A G G A A T G A T A T T C T C A T C A T C T C A T C A T C C C A G G C T G A C T G
A G T T T C T T C A G T T T A C T G A T G T C T G G G T G G G G A C A G A G C C A G A T T C A G A G T A A T C T G
A C T G A A T G G A G A A G T T T C T G C T A C C C C T A C A A A C C C A T G C C T C A C T G A C A G A C C A G C A T
T T T T T T T A A C A C G T C A A A A A A A T A A T C T C C C A G A

FIGURE 194

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9232, pI: 7.94, NX(S/T): 0
MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNGRVQFLHDGSC
```

Signal peptide:

amino acids 1-19

FIGURE 195

CCCGCGCCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC
CGCCGCC**ATG**GCTGCCCTCCCCCGCGCGCCCTGCTGCTCTGGCCCTGACCGGGCTGGCGCTGC
TCCTGCTCCTGTGCTGGGGCCCAAGGTGGCATATAAGTGGAAATAAACTCAAGCTGATGCTCAA
AAACGAGAACGACACTGTTCCAACTAAGACTAAAGTGGCGTTGATGAGAATAAAGCCAAAGA
ATTCCCTTGGCAGCCCTGAAGCGCCAGAACGGCAGCTGTGGGACCGGACTCGGCCCGAGGTGC
AGCAGTGGTACCAAGCAGTTCTACATGGGCTTGATGAAGCGAAATTGAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTAGGCATGGAGGCCAGCG
TCAACTACGATGACTAC**TAA**CCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATT
TCTTCATGTATCTCTTAATGCCTTACACTACTTGGTTCTGATTTGCTCTATTCAAGCAGAT
CTTTTCTACCTACTTGTTGATCAAAAAAGAGACTAAAACAACACATGTAATGCCTT
TGATATTCATGGGAATGCCCTCATTTAAAAATAGAAATAAGCATTGTTAAAAAGA

FIGURE 196

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742
><subunit 1 of 1, 148 aa, 1 stop
><MW: 17183, pI: 8.77, NX(S/T): 0
MAASPARPAVLALTGLALLLLCWGPGGISGNKLKMLQKREAPVPTKTKAVDENKAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNRDRNGHEYGDYYQRHYD
EDSAIGPRSPYGFRHGASVNYDDY
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Signal peptide:

amino acids 1-30

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FIGURE 197

CGGCTCGAGCCCGCCCGGAAGTCCCCGAGGGGCCGCGATGGAGCTGGGGAGCCGGCGCTC
 GGTAGCGCGCGGGCAAGGCAGGC**ATG**ACCCCTGATTGAAGGGTGGGTGATGAGGTGAC
 CGTCCTTTCTCGGTGCTGCCTGCCTCTGGTGCTGGCCCTTGCCCTGGGTCTCAACGCACA
 CCGCTGAGGGCGGGGACCCACTGCCCGACCGTCAGGGACCCCAACGCCATCCCAGCCCAGC
 GCAGCCATGGCAGCTACCGACAGCATGAGAGGGAGGCCAGGGCAGAGACCCCCAGCCT
 GAGACACAGAGGTCAAGCTGACAGCACGCCAGAGCCCAGCAGGGGTTCACAGCAACCCAGCAG
 CCCCGGACTCCCGCAGGAGCCCTCGTGTACGGCTGAAATTCTCAATGATTAGCAGAGCAG
 GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTGAAAAGGACCCAGTTCCGGCCG
 GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCAGCACCCAGACCCCTGG
 GCAGCCTCACCTCCCTCCAACTGCGTTCTCCACTGCCACGTGTCACGAGACTCGGTCCC
 CCAAATCCCCCTGCCCGGGGTCCAGGCCGGCCCTCCGGGCTGGAAATCGCAGCCT
 GCTGCTGCCCTGCTGCTCCTGCTGTTGCTGCTGCTGCTGACTGCCAGATCCAGTACCGC
 CCTCTTTCCCTGACCGCCACTCTGGCCTGGCCGGCTTCACCTGCTCCTCAGTCTCCTG
 GCCTTGCCATGTACCGCCCG**TAGT**GCTCCCGGGCGCTTGGCAGCGTCGCCGGCCCTCC
 GGACCTTGCTCCCCCGCGCCGCGGGAGCTGCTGCCCTGCCAGGGCCGCTCCTCGGCTG
 CCTCTTCCCGCTGCCCTGGAGGCCAGCCCTGCGCCGAGAGGACTCCGGGACTGGCGGAGG
 CCCCGCCCTGCGACCAGCCGGGCTCGGGGCCACCTCCGGGCTGCTGAACCTCAGCCCGCA
 CTGGGAGTGGGCTCTCGGGTCGGGCATCTGCTGTCGCTGCCCTGGCCCCGGCAGAGCCG
 GGCGCCCGGGGGGGCCGCTTAGTGTTCGCCGGAGGCCAGCCGCTCCAATCCCTGAC
 AGCTCCTGGGCTGAGTTGGGACGCCAGGTGGTGGAGGCTGGTAAGGGAGCGGGGAG
 GGGCAGAGGAGTTCCCCGGAACCGTGAGATAAGTAAGTAAACTGTGAAGTTAAAAAAA
 AAAAAAAA

FIGURE 198

MTLIEGVGDEVTVLFSQLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSMRGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVRLKFLNDSEQVARAWPHDTIGSLKRTQFPGRQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS
EPGPSGLEIGSLLLPLLLLLLWYCQIQYRPFFPLTATLAGFTLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

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FIGURE 199

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
 ATTCcccAGGCTCTAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAACAGACCC
 TCAGCTGCACCTCCCTCCCTCAAGGATGAACAAGGGCGCTACTCATCTATTGGTCA
 GAGCTTTCTGCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCA
 GGAGGACTTGGATGGGTTGAGGGTACTCCCTGAGTGACTGGCTGTGCTGGCTTTGTGG
 AAAGCAACTCAACATATCAAAGATAATGAAAATGGGATGGAAGCCTTGACTATGGCCTC
 TTCCAGATCAACAGCCACTACTGGTCAACGATTAAAGAGTTACTCGGAAACCTTGC
 CGTAGACTGTCAAGATCTGCTGAATCCCACCTTCTGCAGGCATCCACTCGC
 AAAAGGA
 TTGTGTCCGGAGCACGGGGATGAACAACTGGGTAGAATGGAGGTTGC
 ACTGTTCA
 CCACTCTCTACTGGCTGACAGGATGCGCCTGAGAATGAACACAGGGTGC
 GGGGTGCA
 ACCGTGG
 AGTCATTCCAAGACTCCTGTCTCACTCAGGGATTCTCATTTC
 TTTCTTCTTCTACTGCCTCCA
 CTTCATGTTATTTCTCCCTCCATTACA
 ACTAAAGCTGACCAGAGCCCCAGGA
 ATAAAG
 TGTTTCTGGCTCCCTTACTCC
 CATCTGGACCCAGTCCCCTGGTTCTGTGTTAT
 TTGTAAACTGAGGACCACAATAAGAAATCTTATATTATCG

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FIGURE 200

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16896, pI: 6.05, NX(S/T): 1
MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSF DYGLFQINSHYW CNDYKS YSENLC HVD CQ DLLNP NLLAGIHC AKRIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCLR
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Signal peptide:

amino acids 1-18

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FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAAGCCCTGCTTGACTGAGAACCCA
 CCAGCTCATCCCAGACCTCTAGACCACTATTATACAAAGGGGAAAGAACACCTGAG
 CAGAATGGAAATCATTATTTTTCCCAGAGAAAACGGGGTAAAGGGAGGGAAAGCAATT
 AATTTGAAGTCCTGTGAATGGCTTCAAGAAGCAATTAAAGAAATCCACTCAGAGAGGAC
 TTGGGGTGAACATTGGGCTCTGTGTTTCTGATGTGAAGTGGAAAGCAGGTCTTGACACGC
 TGTGGCAAATGTCAGGCCAGGAGTAAAGTGCAGGAAAGAAAACCTTCAGGTGGAAACAGCA
 ACCATGTTCTGCTGCAAGCTTGAAGGAGCTGGAGCGGGAGAAAGCTAACTTGAACATGAC
 CTGTTGCAATTGGCAAGTCTAGCAACATGCTCTAAAGGAAGCGATAACAGGCACAGACATG
 CAGACTCCAGTCCCTCTGCTCTGATGCTGGATGCCCTCTGATGATGGTGGCGATGT
 TGCAACCCCTCCCCACACCCACACCGTCAAGACTGTCAAGCAGGCAAGCAGCACAGCC
 GAAGCCAGGTACGGCCTGGACTTGGGGAACTCCAGGATGGGTAECTGGAAAGCTGAGGATGA
 GGGTGAAGAGTAACGCCCTCTGGAGGCCCTGCCACCCCTTATCTCACTGCGGGAGGATCAGC
 TGCTGGTGGCGCTGGCCCTACCCAGGGCAGAAAGGAACAGGCCAGGGCAGGAGGAGTGGG
 AGTACCCGCTCATCAAGGCCAACAGGGCAGGATAAGGAAGCCCCAAAGGGGACTGGG
 GGCTGATGAGGACGGGGAGGTGCTGAAGAAGAGGAGTTGACCCGTTCAGGCTGGACCCAC
 GTGGCTCCAGGAGGCACTCAGTGGCCGCATCCCCCTCCAGGGGCTCTGCCCGAGGTGCGG
 CACCCACTGTGTCAGCAGCACCTCAGGAGCAGCCCTGCCCCAGCCAGCGTCATCTCTG
 TTTCCATGATGAGGCCCTGGTCACTCTCGCGGACTGACAGCATCTCGACACAGTGC
 CCAGGGCCTCTGAAAGGAGATCATCTCTGTTGAGCAGCTCAGCCAGCAAGGACAACATCAAG
 TCTGCTCTCACGGAATATGGCCAGGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAGAG
 GCTGGGTGCCCATCAGGGCCCGATGCTGGGGGCCACAGGGCAGCCACGGGATGTGCTGCT
 TCATGGATGCCACTGCGAGTGCACCCAGGCTGGCTGGAGGCCCTCTCAGCAGAAATAGCT
 GGTCAAGGAGCGAGTGGTATCTCCGGTGTAGATGTTGACTGGAAAGACTTCCAGTA
 TTACCCCTCAAGGAGCCTCAGCGCTGGGGTGTGGACTGGAAAGCTGGATTCCACTGGAAAC
 CTTTCCAGAGCATGTGAGGAAGGCCCTCAGTCAGGCCCCATAAGCCCCATCAGGAGCCCTGTG
 GTGCCGGAGAGGTGGTGGCATGGACAGACATTACTTCAAAACACTGGAGCGTATGACTC
 TCTTATGTCGCTGCGAGGGTGTGGAAAAACTCAGCTGACTGTCTTCAAGGCTGGCTCTGTTG
 GCTCTGGTGAACATCTCCCTGCTCAGGCTAGGACACATCTCACAAAATCAGGATTCCCAT
 TCCCCCTCAGCAGGAGGCCACCTGAGGAACAGGGTTCGCACTGCTGAGACCTGGCTGGG
 GTCATTCAAAGAACCTTCTACAAAGTAGCCAGGCCCTTCAGGCAAGGCTGAGCAAGGCTGAGA
 AGCCAGACTGCATGGAAACCTTGCAGCTGCAAGGAGACTGGGTTGCGACATCTTCAACTGG
 TTTCTGGTAAATGTCACCCATCTGAACCCAGGCCAGTTCCTGCTGAAAA
 GCTCCACAAACACTGGACTTGGCTCTGTCAAGACTGCCAGGAGGAAGGGACATCTGGGCT
 GTCCCATGGTGTGGCTCTTGCAGTGCAGCAGCCGGCAGCAACAGTACCTGCAGCACCCAGC
 AGGAAGAGGAGTACTCTTGCAGGCCACAGCACCTGCTGTTGCTGCAAGGAGGAGG
 GATTCTTCAGAAGTGCACGGAGGAAGGCCATCACCAGCAGCACTGGGACTTCCAGG
 AGAAATGGGATGTTGCCACATTCTGGGAAATGCATGGAAAGCTGGTGAAGAAA
 AATAAAGATTGTCACCTGCCCGTGTGATGGAAAAGCCGGCAGCAGTGCGATTGACCA
 GATAAATGCTGTGGATGAACGATGAACTGCAATGTCAGAAGGAAAAGAGAATT
 AAAATCCAGCTCAAGTGAACGTAAGAGCTTATATTTCTGAAAGCTGATCC
 GTGTGCTCCCTGTGTTAGGAGAGAAAAGCTCTATGAAAGAATATAGGAAGTTCTC
 TCACACCTTATTCATTGACTGCTGGCTGCTTA

FIGURE 202

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
><subunit 1 of 1, 639 aa, 1 stop
><MW: 73063, pI: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLMLGCVLMVMVAMLHPPHHTLHQVTQAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEYEYSPLEGLPPFISILREDQQLVAVALPQARRNQSQGRGGSYRLIKQPR
RQDKEAPKRWDGADEDGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPCLCQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTPVRAFLKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDVLFVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP
VIDVIDWKTFQYYPSKDLQRGVLWDKLDHFWEPLPEHVRKALQSPISPPIRSPVVPGEVVAMD
RHYPQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRRVGHIFYQNQDSHSPLDQEATL
RNRVRVIAETWLGSFKETFYKHSPEAFSLSKAEPDCMERLQLQRRRLGCRTFHWFANVPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMV LAPCSDSRQQYLQHTSRKEIHFGSP
QHLCFAVRQEQQVILQNCTEEGLAITHQQHDFQENGMIVHILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVER
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Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGTCACAGTGAGGAAGACCTCAGACATGGA
 GTCCAGGATGTGGCTCGCTGCTCTGCCCACCTCTCCCTCTCTGCCACTGTGTTG
 TGCCCCCTCCACCCGCTGTGCTAGGGCTCTTCATCTCCCTCGAACCCCCACCAGCCCCAGCC
 CGCCCCCCCCTGTGCCAGGGAGGCCCTCGGCCCCACGTATGTGCGTGTGGAGCAGGC
 ACCTCCACCAAGCCGATCTCTCGGCTCCAAGATCACGTGGCAAGTCTGCCACTG
 CACCCCCCAGCCACCCCATCAGGCTTGAGGAGGGGCCCTCATCCAATACCCCTGGGCT
 ATCTGTGGACTATGGTTTGAGCCCCCATGGGCTCGAACCCCCAACCCCCAACTCAGACT
 CCATGCGAGGTGATGGAGATGGGCTATCTCTGGAGACCTGTGCCACCCCTGCCATT
 CTGTGCGGGCTGGGGAGGGTGTGGACCCCCAGCTCTATGTACAATTACCATCTCAT
 CATCATTTCTCTGTGCCATGGCATCTTCAGGGTCAAGGTGCCCTGAGGCAGGAGGAG
 GACGCAGACCCCTAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGGAGCAGCCACTGACA
 GACCTGCCCCGGCTGGAGCTACTGTGCTGGGGCTCTGGGACTCACCTACCCCCCCCC
 TGACCATGAGGAGCCCCGGGGGACCCCCCTGGGATGCCACCCCCAACCCCCAGGGGCTCCAG
 CCTTCCAGTTGAACCGGTGAGGGAGGGCAATGGGATGGGAGGGCAAAGAGGGAGGCAAC
 TTAGGTCTTCAGAGCTGGGTGGGGTCCCTCTGGATGGTAGTGAGGAGGGCAGGCTGGC
 CTGGCACAGGCCCCCTGGCCCTCCAAAGGGGGCTGGACAGCTCTCTCTGGAGGGCACCTTC
 CTTCTCCCAGTCTCTCAGGATCTGTGCTTATTCTCTGTGCCATAACTCTGCCC
 TCTTTGGTTTTCTCATGCCACCTGTCAAGACAACCTGCCCTCTAACCTGATTCCC
 CCTCTTGTCTGTAACCTCCCTCTATCTGCTGCTACCTGGCTTCTGGTCTGACTGTCCCCT
 TCCCCTTCTCTCTGGATCTCTGTGAAATCTGTGATGCCCTAATGTTGGGTGAGCC
 AAGCAGGAGGCCAACGGGGCCGACAGCCCCCATCCACTGAGGGGGCAGCTGGGGGA
 GCTGGGGCACAGGGGCTCTGGCTCTGGCCCTTGCAACACCCCCGGAAACTCTCCAGCC
 CCACGGCAATCTCTATCTGCTGCCCTCTGGAGGTGGGGCTCACATATCTGTGACTTCG
 GGCTCTGTCCCCACCTCTGGCACTCACATGAAACCCCCACCTGTTCCGAGCCCTTCAC
 AGGCCATTGCAACCGCTCTGCCACCCCTCTCCCGTCCATACCGCTCCGTCAGCTGACTCT
 CATGTTCTCTGCTCTCACATTGCACTCTCTCTCCACATCTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTCTGCACTTAACTCTCTGTGCTTCCGGGCTGATGTTGTTGTTG
 TGTGCGGCGTGTCACTCTCTCATGAACACCCCCACCTGTTCCGAGCCCTGC
 GTGCTGCTCCAGAGGTGGGGAGGTAGCTGGGGCTCTGGGGCTCATGGTCATGG
 TCTCGTCCCACACCATTTGTTCTCTGTCTCCCATCTACTCAAGGATGCCGCA
 TCACCCCTGAGGGCTCCCCCTGGGAATGGGTAGTGAGGCCAGACTTCACCCCCAGCCCA
 CTGCTAAATCTGTTTCTGACAGATGGTTTGGGAGTCGCTGCTGCACTACATGAGAA
 AGGGACTCCCATTGCCCCCTCCCTTCTCTACAGTCCCTTGTCTGTGCTGGCT
 TCTGTGTTGTCCTGCACTCTGGACTCTGAGGCCCCCTGAGCCAGTCTCCCTCCAGCCT
 CCCCTTGGGCTCCCTAACCCACCTAGGCTGCCAGGGACCGGAGTCAGCTGGTCAAGGCC
 ATCGGGAGCTGCTCCAGTCTACCCCTCCCTCCGGACTCCCTCTGCTGCCCTCT
 CCTCCCTCTCTCCACTCTCCCTCTGGCTCCCTGCCCCCTTCCCTCTGGCTCTAGGCT
 CTTCCCTCTCTCACTGGTTTCCACCTCTCCCTCCCTCTTCCCTCTGGCTCTAGGCT
 GTGATATATATTTGTATTATCTCTTCTCTGTGAGTCATCTGAATTACTGTG
 GGATGTAAGTTCAAATAAAGCCTTGCAGATAA

FIGURE 204

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAA\$PQRLRGLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRNSNALSRLVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMN
STINIHRRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 205

GTAAACCAGCGCAGTCCTCCGTGCGTCCC GCCGCCGCTGCCCTCACTCCGGCCAGG**ATGG**
CAT CCT GT CT GG CC CT GCG CAT GG CG CT GCT GG T CT CC GGG G T CT GG CC CT GCG GT G
CTC ACAGACG AT GT TCC ACAGG AG CCG GT GCCC AC GCG T GT GGA AC GAG CC GG CC GAG CT G CC
GTC GGG AGA AGG CCCC GT GG AG AG CAC CAG CCCC GG CG GG AG CCCC GT GG AC ACC GG T CCCC
CAG CCCC AC CG TC GCG CC AGG ACC CG AGG AC AG CAC CG CG CAGG AG CG GCT GG ACC AGG GC
GG CG GG TC GCT GGG G CCG G CT AT CG CG CC AT CG T GAT CG CC G CC CT GCT GG CC AC CT G
CG TGG T GCT GG CG CT CG TGG T CG CG CG T GAG AAG TTT CT G C CT C C **TGA** AG CG A A T A A A
GGGGCCCGCGCCCGGCCGCGCGACTCGGCAAAAAAAAAAAAAAAA

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FIGURE 206

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVAPGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
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Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

GGCGGTTGGTTGGTGC CGCGGCTGAAGGGTGTGGCGGAGCAGCGTCGTTGGTGGCCGGCG
 CGGGCGGGACGGGCA**T**GGCCCTGCTGCTGTGCGCTGGTGTGCGCTACCGCGCGCTGGCCCA
 CGGCTGTCGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
 ACTTCAGTCTGGTGGTGGCGACATCCCCGTGTCAGGGCGCTGCTCACCGACTGGAGC
 GACGACACGATGAAGGAGCTGCACCTGCCATCCCCCAAGATCACCGGGAGAAGCTGGA
 CCAAGTGGCGACAGCAGTGTACCAAGATGATGGATCAGCTGTACCAAGGGAAAGATGACTTCC
 CCGGGTATTCCCCAACGAGCTGCIAAACATCTTCCGGAGCAGGTGCAACCTCATCCAGAAC
 GCCATCATCGAAAGGCACCTGGCACCGAGCTGGGGAGGGAGCTCTCCAGGGAGGG
 ACCCAGCCTAGCACCTGAAGGATCAATGCCATACCCCCCGGGGACCTCCCC**TAA**AGTAGGCC
 CCAGAGGCGCTGGAGTGTGCCACCGCCCTCCCCGAAAGTTGCTCCATCTCACCGCTGGG
 GTCAACCTGGGACCCCTCCCTCGGCCATGGACACACATACATGAAAACCAGGCCAT
 CGACTGTCAGCACCGCTGTGGCATCTTCAGTACGAGACCATCTCTGCAACA**A**CTGACAG
 ACTCGCACGTCGCCCTGCTTGGTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCGT
 GCCAGGGCCCTACTGTCCTGGGTCCCAGGCTCTCTTGAGGGGGCTCCCCGCTTCCAC
 CTGGCTGTCACTGGGTAGGGCGGGGCCGGTGGTCAAGGGCGCACCAACTTCAAGGCTGTGT
 CCCACAGGTCCTCGCGCAGTGGAAAGTCAGCTGTCAGGGCTCCTGAACTACATAAAAC
 TGGCACAAAGTAAGTCCCCCTCTCAAACCAACACAGGCACTGTGTATGTGAGCACCTCGT
 GGTGAGTATGTGTGGGCACAGGCTGGCTCCCTCAGCTCCCACGTCCTAGAGGGGCTCCGA
 GGAGGTGGAACCTCAACCCAGCTCTGCCAGGAGGGCGCTGCACTCTTTCTCCCTAAAG
 GTCTCCGACCCCTCAGCTGGAGGCGGGCATTTCTAAAGGGTCCCCATAGGGTCTGGTCC
 ACCCCATCCCAGGTCTGGTCAGAGCTGGAGGGTCCCTACGATGGTTAGGGTGGCCC
 ATGGAGGGGTGACTGCCAACATTGCTTTCAGACAGGACACGAGCATGAGGTAAAGGCC
 CCTGACCTGGACTTCAGGGGGAGGGGTAAGGGAGAGGAGGGGGCTAGGGGTCTCT
 AGATCAGTGGGGCACTGCAGGTGGGCTCTCCCTACCTGGACACCTGCTGGATGTCAC
 CTCTGCAACACACCCATGTGGTTCATGAACAGACCCACGCTCTCTGCTCTCTGG
 CCTGGGACACAGAGCCACCCGGCTGTGAGTACCCAGAGAAGGGAGGCCTCGGAGA
 AGGGGTGCTCGTAAGCCACACCAGCGTGCAGCGCCATCCAGACATCCCAGGC
 ACGAGGGTGTGTTGGATGTGGCCACACATAGGACCACACGTCAGCTGGAGGAGGGCT
 GGGGCCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
 CCGCAGCCTGGTATGCCAGCCTTAAGGTGTGAGCAGCCCCACACTTGGCCAACCTGACCT
 TGGAAAGTGTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCTGCCCCAGGGCAAC
 GTGGGGGGAGAGACTCAGCTGGACAGCCCTGCCTGTCACCTGGAGCTGGGCTGCTGCTGC
 CTCAGGACCCCTCTCGACAGGGGAGAGCTGAGCTGGCCAGGGCAGGGAGGGGGAGG
 GAGGGAAATGGGGTGGCTGTGCGCAGCATCAGCGCCTGGCAGGTCAGCAGGCTGCGGA
 TGTGATTAAGTCCCTGATGTTCTC

FIGURE 208

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399
><subunit 1 of 1, 157 aa, 1 stop
><MW: 17681, pI: 7.65, NX(S/T): 1
MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSSWWVGDI
PVSGALLTDWSDDTMK
ELHLAIAPAKITREKLDQVATAVYQMMDQLYQGKMYFP
GYFPNELRNIFREQVHЛИQNAIIER
HLAPGSWGGQLSREGPSLAPEGSMPSPRGDLP

Signal peptide:

amino acids 1-15

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FIGURE 209

AGCAGGAGCAGGAGAGGGACA**ATGGAAGCTGCCCGTCCAGGTTCATGTCCTTATTCT**
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAAGTGTGAGAAATCCTCAGATGGTCTG
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCAGCTGCCATGGAATTCAATTGCTGCC
 ACTGAGGTGGCTGTCAAGGCTTCTCCAGGATTAGAAATACCAGCAGTGCCCCACTCCA
 TAGCATGGTGC~~AAA~~ATTCCAGGCGTGCATTGGATCAGCACTGATTGAGGTTCTGA
 CACACTACACATCACTGGAACACCATGCCCTTCCGCTGGTAGACAATGACAACATG
 AATTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAATTGAGCCGTTTCATTGAGAT
 CAACAGCCTCCACATGGTACAGAGTACAACCTGTGACTGTGATTGGTTATTCAACAGCG
 TAATTCA~~G~~ATTCACTCCCTCTGATAATGAACAAGGCCCTCCCAGAGTATGAAGAGAACATG
 CACAGATACCAGAACAGGACGCCAACGCTCTCCAGGGAGATTCTTTATTCTGGACAG
 TGGTATGAAAGAAAATGGAAAGGTGATATCATTTC~~AA~~ACTAAAGGAGTCTCAACTGCCAG
 CT~~T~~GGCAATTAC~~C~~AGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTCC
 GTAGAGCATGTGCAA~~AA~~ACTTTGTGATGGATTCTAAGTGGAAAATTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGAACTCT**GA**CTTCTCCTTGGAACTACATATGGCC
 AA~~G~~ATATCTACTTTATGCAAAGTAAAAGGCACAACTCAAATCTCAGAGACACTAAACACAG
 GATCACTAGGCCCTGCCAACACACACACAGCAGTCACACAGCAGCAGCGTGCACAC
 ACACAGCGCACACACACACACAGAGCTTATTCTCTGCTTAAATCTGTTTCTC
 TTCTCTCTTTAAATT~~C~~ATATCCTCACTCCCTATCCAATTCTCTTATCGTGCATT
 CATACTCTGTAAGCCCCTGTGAAACACACCTAGATCAAGGCTTAAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCAATTGTCATTAAATCAAGT
 TTGTATACTGCACATGACTTACACACACATAGTCCCTGCTTTAAGGTTACCTAAGGGT
 TGAAACTCTACCTCTTCAAAAGCACATGTCCGTCTGACTCAGGATCAAAACCAAAGG
 ATGGTTTAAACACCTTGTGAAATTGTC~~TTT~~GGCCAGAAGTTAAAGGCTGTC~~CC~~AAAGTC
 CCTGA~~A~~CTCAGCAGAAATAGACCATGTGAAACTCCATGCTGGTTAGCATCTCCAAC~~CC~~
 TATGTAATCAACACCTGCATAATAA~~AA~~AGGCAATCATGTTATA

FIGURE 210

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLFLLTCELAEEVAEVEKSSDGPAAQEPPTWLTDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSGFISTDSEVLTHYNITGNTICLFRLVVDNEQLNLEDEDI
ESIDATKLSRPIEINSLHMVTEYNPVTVIGLFNSVIQIHLLLIMNKASPEYEENMHRYQKAA
KLFQGKILFILVDSGMKENKGVISFFKLKESQLPALAIYQTLDEWDTLPTAEVSVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL
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Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGCGGTGGAGGTGCCACCCGGCGGGGTG
 GCGGAGAGATCAGAAGCCTTCTCCCCAACGGCAACCTCAGCGGGACCCGGCTCAGG
 GACCGCGCGCGCGCGCGACTGCAGTGGCTGGAC**GATG**GCAGCGTCCGCCGAGCCGG
 GCGGTATTGCAGCCCCAGACAGCGCGCTGGCTGGTCGGTCTGGCGGCCGCTTGG
 GCTCTGACAGCTGGAGTATCAGCCTTGGAAAGTATATACGCCAAAGAAATCTTGGCAA
 ATGGTACACAAGGGAAAGCTGACCTGCAAGTCAAGTCACTAGTACGACTGGCGGGTTGACC
 TCAGTCTCTGGAGCTTCCAGCCAGGGGGCCACACTACTGTGTCGTTTCCACTACTC
 CCAAGGGCAAGTGTACCTTGGATTATCCACCATTTAAAGACAGAAATCAGCTGGCTGGAG
 ACCTTGACAAGAAAGATGCATCAATCACATAGAAAATATGCAGTTATACACAATGGCACC
 TATATCTGTATGTCAAAAACCTCTGACATCGTTGCCAGCCTGGACACATTAGGCTCTA
 TGTCGTAGAAAAAGAGAATTGCGCTGTGTTCCAGTTGGTAGTGGTGGGCATAGTTACTG
 CTGTTGGCTCTAGGTCTCACTCTGCTCATCAGCATGATCTGGCTGCCCTATAGAAGGAAA
 AACTCTAAACGGGATTACACTGGCTCGAGTACATCAGAGAGTTGTCACCAGTTAACGAGGC
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTGTAAAGAGTCTGCCCTCGGATCTCACC
 AGGGCCCAGTCATATATGACACAGTTAGACCCTCCGGCGGACATCACAGTGACAAGATTAAAC
 AAAGTCAGAGTCTGTTGTATGCGGATATCCGAAAGAATT**AA**AGAGAATACCTAGAACATATC
 CTCACCAAGAACAAAACAACTGGACTCTCGTGAGAAAATGTAGCCCCATTACACATGT
 AGCCTGGAGACCCAGGCAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT
 ACAAAAGGATATGTATAAATATTCTATTAGTCATCCTGATATGAGGAGCCAGTGTGATGA
 TGAAAAGATGGTATGATTCTACATATGTACCCATTGCTGTGTTTGTACTTCTTTTC
 AGGTCAATTACAATTGGGAGATTTCAGAAACATTCTTCACCATATTAGAAATGGTTG
 CCTTAATGGGAGACAATGAGCAGATCCTGTAGTATTCCAGTAGACATGGCCTTTATCTAAG
 GGCTTAAGACTGATTAGTCTTAGCATTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
 GCATACCCAGGGTGGCCTTGTACAGTATCAGTACCATTTATGTCTGCCGTTTAAAAA
 AATACCCATTGGCTATGCCACTTGTAAACAAATTGAGAAGTTTTTGAGTTTCTCACT
 AAAATATGGGCAATTGTTAGCCTTACATGTTGTAGACTTACTTTAAGTTGCACCTTG
 AAATGTTGTCATCAATTCTGGATTCTAACATAGCAAGATTAGCAAAGGATAAATGCCAAG
 GTCACTTCATTCTGGACACAGTTGGATCAACTGTATAAGTAGAAAATCCAAGCTTGT
 GAGAACTTTGTAACGTGGAGAGTAAAAGTATCGGTTTA

FIGURE 212

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510
><subunit 1 of 1, 269 aa, 1 stop
><MW: 29082, pI: 9.02, NX(S/T): 3
MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKKDASINEN
MQFIHNGTYICDVKNPDIIVVQPGHIRLYVVEKENLPVFPVVVVVGIVTAVVVLGLTLLISM
LAVLYRRKNSKRDYTGCSTSESLSPVKQAPRKSPSDTEGLVKSLSPGSHQGPVIYAQLDHSG
GHHSDKINKSESVVYADIRKN
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Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

FIGURE 213

GCCGGCTGTGCAAGAGACGCC**ATG**TACCGGCTCTGTCAAGCAGTGA
 CTGGGGGGCTGGCCTCAAGCTGCGGACCGACGCGGGGTCATCAGCGCGCCGGCTGCCGCC
 TCTCGGCCACGGCTGGGCTGGGGGCTCGGGCTGGGCTGGGGCTGGCGCTGGGGTGAAGC
 TGGCAGGTGGGCTGAGGGCGCGCCCCGGCGAGTCCCCCGCGCCCCCGACCTGAGGCG
 TCGCCTCTGGCCGAGCCGCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCGGC
 GCCGCCCTGCTCCAGGTCTCGCCAGAGCCATCGAGAGCAGCCGACCTGTCACAGGA
 TCAAGGATGAGGTGGCGCACCGGCATAGTGGTTGGAGTTCTGTAGATGGAAAAGAAGTC
 TGGTCAGAAGGTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAACACAGAGACAGT
 TATGCAATTGCTAGCATCAGAAAGTCTCACCATGGTGTCTTGC
 CAAATTGTTGGAA
 CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTC
 CCAAGTGGAAATTCCCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTCTGTCAACAAGATTACTGATTTCCATTAA
 AGTGGAAATTTCG
 TCATTATGAAAAGGACATAAAAAGGTGAAAGAGAGAAAGCTTATAAGCCTTGAAGATGA
 TGAAAAGAGAATGTTGCTATTGAGCAAGAAAAGAAGGCAAAGTAATGAAAAGAATGATT
 ACTAAATTAAAACAGAGCAGGAGAATGAAGCCAATGCCGAATTCAAAACCTG
 GCAAGAA
 AAAAGAATGATTTGAACAAGGCGAATTATATTGAGAGAAAAGTTGAAAATTCAATTGAAT
 CCCTAAGATTATTTAAAATGATCCTTGTCTCAAACTGGTAGTCAGTTTG
 TATTCA
 ACTTTGGCTATAACCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATG
 TAAATATTGGA
 CTATATGCAAGAAAATATTCCATGACTTGGATATGCTGACGACTGTG
 CAGGAAGAAAACGAGC
 CAGTGATTACAATAGAGCAAGG**TA**ATGAATACCTTCTGTGTAGCTATATCGC
 ATC
 TTAACACTATTTATTAAATTAAAAGTC
 AATTTCTTGTGTTCCATTCAA
 AACCTGC
 CACATTGGGAGCTTTCTACATGCTGTTCTCATCTG
 TAAAGTGAAGGAAGTAAAACA
 TGTTTATAAAGTAAAAAAA

FIGURE 214

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAPGGLASSCGRRGVHQAGLPPLGHGWVGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPQEQSLAPWSPQTAPPSCRCFARAIESSRDLLHRIKDEVGA
PGIIVGVSVGDKEVWSEGLGYADVENRVPCKPETVMRIASISKSITMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKNDFEQGELYLREKFENSIESRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRAR
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGATGCACGCGTACGTAAGCTCGGAATTCCGGCTCG
 AGGCTGGTGGGAAGAAGGCCGAGATGGGCGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCCTG
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGGCCGGGGCAGCGGCTGCCGGCCGGGACT
 GGTGCGCGAGGGGCTGGGGCGGAAGGTGCGAGAGGGCGAGGGCTGTGGCACGGTGGGCTGCT
 GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACCTCCGGAAAGCGGGCTACTGCTCT
 GGAACCACCGAGGATGGTACCTGTCCCTGTACAGCGCAGCTCAGCGAGGAGGACGGGGC
 CGACTCCGGGATGTGGCAGCCCTGAATGCCCTGTACCGGGTCCGGATCCCAAGGCAGCCGG
 GGCCCTGGATGGCCTGGAAAGCTGGTGGCTATGTCTCCTCTTGTCCTGCGTGTCCCCTGG
 TGGAGTCGCACCTGTGCGGACCAGCTGACCCCTGCACGTGGATGTGGCCGGCAACGTGGTGGG
 GTGTCGGTGGTACGCACCCGGGGCTGCCGGGCCATGAGGTGGAGGACGTGGACCTGG
 GCTGTTCAACACCTCGGTGAGCTGAGCCGCCACACAGCCCCAGGCCCTGAGACGGCG
 CCTTCATTGAGGCCCTGGAGATGGAACAGGCCAGAAGGCAAGAACCCCAGGAGCAGAAG
 TCCTTCTTCGCCAAATACTGGATGTACATCATTCCCGTGTCCCTGTTCTCATGATGTCAGG
 AGCGCCAGACACCGGGGGCAGGGTGGGGTGGGGTGGTGGTGGGGTAGTGGCC
 TTTGCTGTGTGCCACCCCTCTGTAAGCTATTAAAAACATGACGATACTGTTGTTGGCAAGACGG
 TGAACGTTTGGAAAGCTACAGCTCCAGCAGCAGCAAAGCAACTGTTGTTGGCAAGACAG
 TCTTGATGTACAAGCTTGATTGAAATTCACTGCTACTTGTACGTTATTCAAGAAACCCAAAG
 GAATGGCTGTCCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGGCAGTTTAT
 TAAACTGTCCCCAGATCGACACGAAAAAAAAAA

FIGURE 216

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529
><subunit 1 of 1, 269 aa, 1 stop
><MW: 28004, pI: 5.80, NX(S/T): 1
MAAASAGATRLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAAALNGLYRVRIPRRPGALDGLEA
GGYVSSFVPACSLVESHLSDLTLLHVDVAGNVGVSVVTHPGCGRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEOKSFFAKYWMYIIPVVLFLMMMSGAPDTGGQ
GGGGGGGGGGGGSGLCCVPPSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT
 GGAGCCGGACGTGTCGGGCGTCCCCCAGACCGGGGAGCAGGTGCTCCGGGGCCACC
ATGCTGGTACTGCCACCTTGCTTTGTAGGCCCTCTGGCCTCCTGCCCTGGGCTGGAACCT
 GTCAAGATGCCGGCTAAACCCCTGGAAAGGGCCTGCAGCAATCCCTCCTTCCTCGGTTTC
 AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTCAGGCCCTAC
 CTCTATAAAACTCTACCAAGCATTACTACTTCCTGGAAAGGCAAATTGCCATCCTCTATGCTG
 TGGCCTTGCCCTACAGTCCCTTGGCCTAGTGGCCTCCCTTGTTGGATTGGCTGGTC
 GCAAGAATTCTTGTCCTCTCCCTGACTTACTCACTATGCTGCTAACCAAATCTCT
 CAAGACTACTTGTCGCTGCTAGTGGGGCGAGCACTGGTGGGCTGTCACAGCCCTGCTCTT
 CTCAGCCTTCAGGGCCTGGTATATCCATGAGCACCTGGAACGGCATGACTTCCCTGCTGAGT
 GGATCCCAGCTACCTTGCTCGAGCTGCCCTCTGGAAACCATGTGCTGGCTGTAGTGGCAGGT
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGCGTAGCGCCCTTGTGGCTGC
 CATCCCTCCTGGCTCTGGCAGGGGCTTGGCCCTCGAAACACTGGGGGAGAACTATGACC
 GGCAGCGTGCCTCTCAAGGACCTGTGCTGGAGGCCTGCCTGCCTCTGCGACGCCGC
 GTGCTGCTGCTGGCACCATACAAGCTCTATTGAGAGTGTCTCATCTTGTCTCCCT
 CTGGACACCTGTGCTGGACCCACAGGGGCCCTCTGGCATTATCTCTCCAGCTCATGG
 CAGCCAGCCTGCTGGCTTCCCTGACCGTATGCCACCTCCAAGAGGTACCACTTCAG
 CCCATGCACCTGCTGCCCTGCTGTGCTCATCGTGTCTCTCTCTCATGTTGACTTT
 CTCTACCAGCCCAGGCCAGGAGAGTCGGTGGAGCTCCCTCATAGCCTTCTACTTATTGAGT
 TGGCTGTTGAGATTACTTCCCAGCATGAGCTTCTACGGAGAAAGGTATCCCTGAGACA
 GAGCAGGCTGGTACTCAACTGGTCCGGTACCTCTGCACTCACTGCCCTGCTAGGGCT
 CCTTGTCCCTCATGACAGTGTGAAACAGGCACTCGGAATATGTTGAGCATTTGCTCTG
 CTGTCATGGTGTGATGGCTCTGCTGGCAGTGGTGGACTCTCACCGTGGTAAGGCATGATGCT
 GAGCTGCGGGTACCTCACCTACTGAGGAGCCATGCCCTGAGCTG**TAACCCCAC**TCCAG
 GACAAGATAGCTGGACAGACTCTGAAATTCCAGCTCCGGATTGACAGATCTCTGT
 GACTGACTTTGTGACTGTCCTGTGGTTCTCCTGCCATTGCTTGTGTTGGAGGACATGA
 TGGGGGTGATGGACTGGAAAGAGGTGCCAAAAGTCCCTCTGTTACTCCATTAGAAA
 ATAAACACTTTAAATGATCAAAAAAAAAAAAA

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
QDYFVLLVGRLAGGLSTALLFSAFEAWYIHEHVERHDFFPAEWIPATFARAAFWNHVAVVAG
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGNEYDRQRASFRTCAGGLRCLLSDRR
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFFSFMAASLLGSSLYRIATSKRYHLQ
PMHLLSLAVLIVVFSLFMLTFSTSPQESPVESFIAFLIELACGLYFPSMSFLRKVIPET
EQAGVLNWFRVPLHSACLGLLVLHDSDRKTGTRNMFSCSAVMVMALLAVVGLFTVVRHDA
ELRVPSPTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGCGGGCGGGCGAGAGGAAACGCGGCCGGGCCGGGCCCTGGAG**ATG**
 GTCCCCGGCCCGCGGGCTGGTGTGTCGTCTGGCTCCCGCGTGCCTCGGGCC
 CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGACATTGATACA
 TCTTCACAGCCACACCTGCAAGGACTTGGTGTATCTTCACACAAGGTATGAGCAGATT
 CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACTCAGCAACGGTTCTCATCCA
 GGACCAAGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTCTCCAAGACTCGGGTGTCC
 AGGAGCACGGGGCGGGCGGTGATCATCTGACAACGCAGTGACAATGACAGCTTCTAC
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTTCTGCTCGG
 CCGAGACGGTACATGATCCGCGCTCTGGAACAGCATGGGCTGCCATGGGCCATCATT
 CCATCCCAGTCATGTACCAGCATCCCCACCTTGGACTGCTGCAACCGCCCTGGACCTTC
 TGG**TAGA**AGAGTTGCTTCAACATTCCAGCCATAAGTGACTCTGAGCTGGAAAGGGAAACCC
 AGGAATTGGTCACTTGGAAATTGGAGATAGCATCTGGGACAAGTGGAGCCAGGTAGAGGA
 AAAGGGTTGGCGTTGCTAGGCTGAAAGGGAGGCCACACCCTGGCCTTCCCTCCCCAGG
 GCCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCAGGGCTCTGGCTA
 GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGGCCATCTGTGACCTGTCACACT
 CACCTGGCTCCAGCCTCCCTACCCAGGGTCTGTCACAGTGACCTTCACAGCAGTTGG
 AGTGGTTAAAGAGCTGGTGTGGACTCAATAACCCCTACTGACTTTTAGCAATAAA
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAA

FIGURE 220

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCVLWLWPACVAAHGFRIDHYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHHGRAVIISDNADVNDSF
YVEMIQDSTQRTADIPALEPLLGRDGYMIRRSLEQHQHGLPWAIIISPVNNTSPTFELLQPPTFW
```

Signal peptide:

amino acids 1-20

FIGURE 221

TCTGGCTCCACTGCTGTGCTGGGATC**ATG**GAACTTGCACTGCTGTGGCTGGTGA
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG
ACTGGGAAAATGCCATCCTCTCTACTGGCCCTACGGCTGTACTGCGGACTAGGTGGCAG
AGGCCAACCCAAAGATGCCACGGACTGGTGTGCCAGACCCATGACTGCTGTATGACCACC
TGAAGACCAGGGTGC~~GG~~CATCACAAGGACAACAAAAGCAGCATACATTGTATGGAT
TTATCTCAAGCTATTGTTAATGGCTGTGTTAATGTGATCTATCTGGAAAATGAGGACTC
CGAAT**AAA**AGCTATTACATWTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 222

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCCHCGLGGRGQPKDADW
CCQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDLSQRYCLMAVFNVIYLENEDSE
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGTTCTCCTCTGGATGGGGCCAGGGGCCAGGAGAGTATAAGGCATGTGGAG
GGTCCCCGGCACACCAGACGCCAGTCACAGCGAGAGCCCTGGG**ATG**CACCGGGCAGAGG
CCATGCTGCTGCTGCTCACGCTTGCCTCCTGGGGCCACCTGGCAGGGAAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTCAGCACCCTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTGCTGTAGGTCTCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTAGGTGGAAATACCCAGGAAGTCACCTGCAGCCAGGGAAATAC
ATCACAAAAGTCTTGTCGCCTCCAAGCTTCCCTGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTCTATTGGAGCTGATGCCAGATCTCCTGCCTACCCAGCCAAG
AGGGCAGGTGCTGGTGGCATCTATGCCAGTATCAACTCCTGGCATCAAGAGCATTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACACTGAGCCACCAGTTAATCTCACATACTC
AGCAAACTCACCGTGTTGCG**TAGGGTGGGTATGGGCCATCCGAGCTGAGGCCATCTGT**
GTGGTGGTGGCTGATGGTACTGGAGTACTGAGTCGGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTCTGCAGAAAA

FIGURE 224

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLKVSVQVK
LGDSWDVKGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGKSIGFEWNYPLEEPTEPPVNLTYSANSPVGR
```

Signal peptide:

amino acids 1-22

{ 1
{ 2
{ 3
{ 4
{ 5
{ 6
{ 7
{ 8
{ 9
{ 10
{ 11
{ 12
{ 13
{ 14
{ 15
{ 16
{ 17
{ 18
{ 19
{ 20
{ 21
{ 22

FIGURE 225

GCTGAGCGTGTGCGCGTACGGGCTCTCTGCCCTCTGGGCTCAACGCAGCTCTGGCT
 GAACGGGTGCTCATCACGGGAAGCTGCTGGCTATGGAAATCAGATGTGGCAGTCAGTAG
 CCCAAGGAAATTGCGCTGGAAAGAACATCATGTTTCTGATAAGAAGAAATTGAGGATCCAGTT
 TTTTTTTAACCGCCCCCTCCCCACCCCCAAAAAAACTGTAAGATGCAAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTTGATGTTTCTGCGAATGCGGTGTTGGGATT
 TATTGTTCTGGAGGTGTTCTGGCTGGCAAAGAAATAATGTCAGGAAATTGCGTCCATCT
 CCCAAGGGGCTCCAATTCTTCTGGGTGTCAGCGAACCTGACTCACTACAGTCAGCTG
 ACAGGGGCTGTATGCAACTGGCCCCTAACGCCAACGAAAGACCTAACAGACGACCTTGAA
 CAATACAAGG**ATGG**TTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCACTGCTTACTGAAATGCTTCTCCGCGAACGAGGGATGCGCTAAAGGCTG
 TAGGTGTAAGGCAAATTGGTATATTGTAATCTCAGAAATTACAGGAGATACCCCTAAGTA
 TATCTGCTGGTGCTTAGGTTGTCCTCTCGCTATAACAGCCTTCAAAACTTAAGTATAAT
 CAATTAAAGGGCTAACACAGCTACCTGCTATAACCTGACCATTAACCATATCGAACATAT
 TGACGAAAATTGCTTTAATGGAATACCGCAGACTAACAGCTGATTCTTAGTCCAAATAGAA
 TCTCTATTCTTAACATACCTTCAGACCTGTGACAATTACGGAATTGGAATTGGATCTGTCC
 TATAATCAGCTGCAATTCTGGGATCTGAACTGTTTCCGGGCTTGCGGAACGCTGCTGAGTTT
 ACATTTACGGCTTAACCTCTGGAAACCATCCCTGCGAATATTCCAAGACTGCGCAACC
 TGGAACTTTGGACACTGGGATATAACCGGATCTCGGAAGTTAGCCAGGAATGCTTCTGGC
 ATGATCAGACTCAAAGAACCTCACCTGGAGCACAATCAATTTCAGCTAACCTGGCCCT
 TTTGGACAGTTGGTACGGCTTACAGGAACCTTACTCTGAGTGGAAATTAAACTCAGTGTCAATAG
 GAGACGACCATGCTCTGGACACTGGGCTTACAAAGGCTTGATTATCAGGCAATGAGATC
 GAAGCTTCAGTGGACCCAGTGTTCAGTGTGTCCTGAATCTGAGCGCTCAACTTGGG
 TTCAACAAAGCTCACATTATTGTCAGGAGATTGGGATTCTGGATATCCCTCAATGACA
 TCAGTCTGCTGGGAAATTGGAATCAGCAGAAATTGCTCCCTGTAAACTGGCTG
 AAAAGTTTAAGGTCTAAGGGAGAAATCAATTATCTGCGCAGTCCAAAGAGCTGCAAGG
 AGTAAATGTGATGAGCTGAGTAAGAACACTACAGCATCTGTCAGGCAAAGTACTACAGAGGGT
 TTGATCTGGCCAGGGCTCCCAAAGCCGACGTTAACGCCAAGCTCCCCAGGCCAGAC
 GAGACCAAACCCCTTGGCCCCAGCGTGGGAGCACAAGGCCAGGCCAGAGACGATGC
 TGACGCCGAGCACATCTTCCATAAAATCATCGGGGAGCGTGGCCTTCTGTCCG
 TGCTGCTGAATGGACGGGACCCCTGCACCTATAACAAATCGGGCTCAGGGAGTGTAGGTA
TGAACCATTTGATAAAAAGAGCTTAAAGCTGGGAAATAAGTGGTCTTATTGAAC
 TGCTGACTATCAAGGGAAACGCGATGCCCTCCCTCCCTCTCCCTCACTTTGTTG
 CAAGATCCCTTGTGCTTTACTGCAATTATACTGGTATTTCCTCTCATACATA
 ATCAACCCATTGAAATTAAACACAAATCAATGTAAGGCTGAAACTCCGGTTAAATATAA
 TACCTATTGATAAGCCCTTACTGATTCCATTAAATGTCGATTTAGGTTAAAGATAAAACT
 TCTTCATAGGAAAAAAAAAA

FIGURE 226

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGKMYCSESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRI FQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKELHLEHNQFSKLNLAFLPRLVSLQNLYLQWNKISIVGQTM
SWTWSLQRDLISGNEIEAFSGPSVFQCPVLQRNLDSNKLTFIGQEILDWSISLNDISLA
GNIWECSRNCISLVNLKSFKGLRENTIICASPKELOGVNVDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLSMRKKRQSLKQMTPSTQE FYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCTGAGAAAGAAGGAATAAACACAGGCACCAACCCACTATCCTAAGTTGACTGTCCTT
 TAAATATGTCAAGATCCAGACTTTCAGTGTCAACCTCAGCGATCTCAACGATAGGGATCTG
 TGTTGCCGCTATTCCAGTGGTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTG
 AAATTATAATGACCAACACCCATAATGGCTGGTATATCTGGATCCTCTGCTGCTGGTTTGG
 TGGCAGCTCTCTGTGGAGCTGTGGCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA
 ATTGATTCTCACAGGGCACCATGGCAGTTTTGCTGTTGGAGACTTGACTCTATTATGG
 GACAGAAGCAGCTGTGAGTCAAACGTGTTGAATTCACCTCAAACCTAAACCCCTGACCTAT
 ATCCGTCTCTGCTCCATGTTGGCCCTTAGGCTCCCCACCTCATATGAAGAAATTGTA
 AAAACAACTGATTTAGGTGTGGATTATCAATTAAAGTATTAAACGACATCTGAATTCCA
 AAACATCAAATTAGGAATAGTTATTCAGTTGTTGAAATGTCAGAGATCTATTATCATA
 GTCTGAGGAAGGACAATTGCAAAAAGAATGGATGTTGGAAAAAATTGGTCATGGAGATG
 TTAAATAGTAAAGTAGCAGGCTTTGATGTGTCAGTGCTGTATCATACTTTATGCTACAC
 AACCAAATTAAATGCTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
 TCCATCACATTAGGACTCCACTGCGATACAGCACACCATTCTGCTTAAACTCTTC
 CTAGCATGGGGTCCATAAAAATTATTATAATTAAACATAGCCAAAGCCGAGAATCCAACAT
 GTCCAGAACAGAACCAAGAGATAGTATTGAATGAAGGGTGAGGGGAGAGAGTAGGAAAAA
 GAAAAGTTGGAGTTGAAGGGTAAAGGATAATGAAGAGGAAAGGAAAGATTACAGTCT
 CAGCAAAACAAGAGTTTATGCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGAGAAAAGAAAATTCCC
 CTTTACAGTAATGAATGTGGCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTG
 GCATTATTGGCAGCATCTGCTAAGAACCTCGGCATAGGTATCTGTTCCATGAGGACTGC
 AGAAGTAGCAATGAGACATCTCAAGTGGCATTGGCAGTGGCCTCAGCAGGGGACAGA
 CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTGTTGAACAAAACAAT
 AAACATCAATAGATATCTAAAAA

FIGURE 228

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
><subunit 1 of 1, 146 aa, 1 stop
><MW: 16116, pI: 4.99, NX(S/T): 0
MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCEEDEMCVNNDQHPNGWYIWILLLVLA
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPVTVGIGHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT
```

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGCGGGAGTAAATCTCCACAAGCTGGGAACAAACCTCGTCCC ACTCCCACCCACGGCGT
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCACTGTGGGAGCCAGCTGACGCCCTTATTAA
 GCTCTCGCTGGCTGCCCGCTCAAGAACCTCCCTGGCGGCCGACCTGACGAGAACCCC
 ACGGCCAGCTCAGTTCTCTACTTGGGAGAGAGAGAAAGTCAGATGCCCTTTAAACT
 CCCCTCTCAAACATCATCTCTGGCTGACTGACTTAATAGAGTGGATAACACCTTGTGAAG
 ATGAAGAATATACAATATTGAGGATTTTTCTTTTTCAAGTCTTGATTGTGGC
 TTACCTCAAGTACCATTTCTAGTCAGTCTGTGTTCTTCAGAAATGTTTA
 CAATCTCAAGAAAAATATGTCAGAAATTGAGTTACTGTTGTTGATTGGACTCATT
 TGGGGATTGATGTTACTGCACTATACTTTCAACAAACCAAGACATCAAAAGCAGTGTCAAGTT
 ACCTGAGCAAACTAGACTAGAAAGCAGTGTAAAGCTTAGCAGAGGAAAATAAGA
 ACACAGTGGATGTCGAGAACGGTCTCTATGGCAGGATATGCCGATCTGAAAAGAACATT
 GCTGTCCTCTGGATGACATTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT
 TGTGTGAATGGCTCAGGCCAACACCCAACTGGTACTGTGGAGAATTGGTCCAGTAA
 CCACAAATAAAAGAACGAATGTCGCGCAGTATCAGAATAGCAGTTGAAAATCACCTGTGC
 TGTCATCCACTGTTGATTATCCTATGGCAGAAAAGCTTATAATTGCTGGCTTAGGAC
 AGAGCAATACCTTACAATAAAAGCTCACACATTTCAGGAGTATGCTGGATTCTGGAAAC
 CTCTAATTCTGTCACATAAAATTTAAAGTTATGTTGCTTTCAGGCAAGTCTGTCATG
 CTGACTATGTCCTTAAAGAGATTGGTAACTTGTGATGTTGAAAGCAGATAGGTGAGT
 TTTGTATAAACTTTGTGTTGAGATCAGCTGAAATGAAAACACTGAAAACATGGATT
 ATTTCATACACATTATAAGTATATAACAGCTTTGGACAAGTGAAGAATTGTTAA
 TCATTCTGTCATTGTTCTCAATAGATGTAACTGTAGACTACGGCTATTGAAAAAATGTG
 CTTATTGTACTATATTGTTATTCCAATTATGAGCAGAGAAAGGAAATATAATTGTTAAAA
 TAATGTTTGAAATCATGACCCAAAGAACATGATTGATTGCACTATCCTCAGAAACTCTGA
 AGGTAAATTGTTGATATTAAATACATTAAGGATATAATTGTAATGGTAG
 CGCCACTGTGTCATTACCTATCGTAAACATTGGGCAATTAAATACAGCATTAAGGTT
 GTAAACTCTAACTTAACTTATTGAGAAATAAGGATATTGATGAGAGTAACAATA
 AAAGTATTGATTTGACATACATGAAATGTTGTCATTAAAGGTTAAATCCTTGAGTGTCT
 ATGCTATCAGGAAAGCACATTATTCATATTGGTTAATTGCTTTTATTATGGTC
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTGAGGACTTTAGCCAGGTGATATAATAAA
 GGTACTTTGTGTCGATTAAATTGCTGGAAAGTGTAACTTATTATATAAGAGTATC
 CTTTATGAAATTGAGATTGATATAACAGATGCAATTAGATATTGATTTTATATAATTGCCCAC
 TAAATAAAAGAACATTAAATATAACATGAAAGATGACTATCTTCAGGAAAAAGCT
 GTATATAGCACAGGGACCCCTAATCTGGTAATTCTAGTATAAAACAAATTATAACTTTAT
 TTAATTTCCCTTGAGCAAACTAATTGCCACATGGTGCCTTATTTCTAGTATTGTT
 CTCTATAGTAACTGCTTAAGTGCAGCTAGCTTAGATTAGACTATATAAGAATTAGATAT
 TGATTGTTGTCATTATAATGTCACACATGAGCAATAATTACAATATTGTTTATTA
 TAAATATGAGAAATATTGTTCATGAAAGACAGATTCCAAATCTCTCTCTCTGT
 CTGTCACCTTATGAGAAATTAAATTATGCCCCAGGT

FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADILKRTIAVLLDDILQRLVKLENKVVDYIVVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR
```

Important features of the protein:

Signal peptide:

amino acids 1-26

1
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FIGURE 231

CGCGGGCCGGGCCGCGGGGTGAGCGTGCAGGGCGCTGTGGCGCAGGCTTCAGCCCCAC
 C**ATG**CCGTGGCCCTGCTGCTGCTGCTGGCCGTAGATGGGCCAGACAACCCGGCATGCT
 TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCTTTTCGACAGCTTCAGCTGACTCGG
 GTGGATGTAGCGGCTGGGCCCCACATGCGGCTGCCATCCCTTGACACAGCCA
 CTTGGACCTGTCTCCAACCGCTGGAGATGGTGAATGAGTCGGTTGGCGGGGCCGGCT
 ACACGACGTTGGCTGGGATCTCGACACCCAGCTCACCCAGCATTCACCACATGCTCC
 TTCTCCGCCTTCGCTACCTGGAGTCGCTGACCTCAGCCACATGGCTGACAGCCGCCC
 AGCCGAGAGCTTACCAAGCTCACCCCTGAGCGACGTGAACCTTAGCCACAACCAGCTCCGGG
 AGGTCTCAGTGTCTGCCCTACGACCCACAGTCAGGGCCGGCACTACACGTTGGACCTCTCC
 CACACAGCTTACCCAGCTCGTGGCCACCCAGGGGCCGGCTGCGCTGCGCCACCAT
 TCAGAGCTGAACCTGGCTGGAGCTCCATGGCTGCCAACCTCCGAGACTTGGCC
 TGCGTACCTGAGCTGGATGGAAACCTCTAGCTGTCATTGGTCCGGTGCTTCGCGGG
 CTGGAGGGCTTACACACTGTCTGCCCTGAGCTGGAGCTCCCTGAGCTGGCGCCAG
 TGGCTTCCGTGAGCTACGGGCTCGAGGCTCTGGACCTGTGCGGCAACCCCAAGCTTAAC
 GGGCAGGAGCTGAGGTGTTTCAGGCTTAGCTCCCTGAGGAGCTGGACCTTCGGGACC
 AACCTGGTGGCCCTGCCTGAGGCCTGCTCCCTCACCCCGGCACTGAGAGCTGAGCGT
 GGGCAGGATGTGGCTGGCCGGCGCCCTGGTGGGGAGGGCACTACCCCGGAGGGCTGGCT
 CAAGCCCAAGTGGCCCTGACTGCGTAGACACCCGGAACTCTGCTGCGAGGGGGCCACC
 ATCTGT**TGACA**ATGGTGTGGCCCAGGGCACATAACAGACTGCTGTCCTGGCTGCCTCAG
 GTCCGGAGTAACCTATGTCATGTGCAACACAGCTGGGAGGCCAGGGCTATGTGCA
 GCGTACCCACAGGAGTTGGGCCCTAGGAGAGGCTTGGACCTGGGAGGCCACACTGGAGC
 AAAGCTCACCCCTTGTCTAGCTGCTCCCTCACCATGAGCAGAGGGACTTCGATGCCA
 AACCAAGACTGGGTCCCCCTCTGCTTCCCTCCCCACTTATCCCCAAGTGGCTTCCCTCAT
 GCCTGGGGCTGGCTGACCCGGCAATGGGAGGGTGGGGACCCCTGCTGCGAGGGCAGA
 GTTCAAGTCACTGGGCTGAGTGTCCCCCTGGGCCATGGCCAGTCACTCAGGGGAGATT
 TCTTTCTAACATAGCCCCTTCTTGCATGAGGCCATGAGGCCGCTTCATCCTTTCTAT
 TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAAGATCAAGTCCACCCCTCTCATGTGAC
 AGATGGGAAACTGGAGCTTGGAGAAAAGGCTTAATCTAAGTTCCTGCGGGCAGTGGC
 ATGACTGGAGCACAGCCTCTGCTCCAGCCGGACCCAATGCACTTTCTGTCTCTCTA
 ATAAGCCCCAACCTCCCCCTGGGCTCCCTGGCTCCCTGCTGCCCTGGGACCCCTGCT
 GGAGTAGCAGCAGGACAGGCAAGGCTCACAGTGGGACTCTGGGCTCTGACAGCT
 GTGCGCATGGCTAAGTCCTCTGCCCTGGGCTTGGGACTCTGGAAAGCTTAGGGCACATTGGT
 CCAGCCTAGCCAGTTCTCACCTGGGTGGGGTCCCCAGCATCCAGACTGGAAACCTACC
 CATTTTCCCCTGAGCATCTCTAGATGTCAGGGCCCAAGGGAGTTGCTGAGTTCTGGAGCCTCA
 TCTGGCTGGGATCTCAAGGGCCCTGGGATTCTGGCCACTGGGCTGAGCACAGC
 CCTTCTACCCCTCCAGGAATGCCGTGAAAGAGACAAAGTCTGCCGACCCATGCTATGC
 TCTACCCCAAGGGCAGCATCTCAGCTGGGACTCTGGGCTTCTTCTAGTCTTCATTTA
 TAAAAGTTGGCTTTAACGGAGTGTCACTTCACCCGGCTCCCTACCCCTGCTGGC
 CGGGGATGGAGACATGTCTTGTAAAGCAGAAAAGGTTGCAATTGTTCACTTTGTAAT
 ATTGTCTGGGCTGTGTTGGGTGTTGGGGAGCTGGCAGTGGACTCTGCTTCCCCCACCTGCTAGC
 CCATCATCTATCAACCGGTCTTGTATTAAACATATAAAAGGTTAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 232

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPPLLLAVSGAQTTRPCFPGCQCEVETFGLFDSDLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTAPE
AESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHVDLSHNLIHRLVPHPTRA GLPAFTI
QSLNLAWNRLHAVPNLRDPLRLYSLDGNPLAVIGPGAFAGLGGLTHLSLASLQRPELAPS
GFRELPGHQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLHLHPALQSVSV
GQDVRCRRLVREGTYPRRGSSPKVPLHCVDTRESAARGPTIL
```

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCACGCCACAGCTCTGTGAGATTGATTTCTCCCCAGTCCCCGTGGGTCTGAGG
 GGACCAAGGGTGAGCTACGTTGGCTTCTGGAAGGGAGGCTATAATGCGTCATTCCCCA
 AAACAAGTTTGACATTCCCCTGAAATGTCAATTCTATCTATTCACTGCAAGTGCCTGCT
 GTTCCAGGCCCTAACCTGCTGGCACTAACGGCGGAGCAGGATGGGACAGAATAAAGGAGC
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTGAAATCTCTTCAC
 GGGAGGCTGGCAGTTTCTACTCCTGTGGCTCCAGATTCAGGCCAAAGATGAAAGCC
 TCTAGTCTTGCCTTCAGCCTCTCTGCTGCCTTATCTCTATGGACTCTTCCACTGG
 ACTGAAGACACTCAATTGGGAAAGCTGTGTGATGCCACAAACCTTCAGGAAATACGAAATG
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAAATCTTA
 AGGAGGACTGAGTCTTGCAGACACAAAGCCTGCGAATCGATGCTGCCTCTGCCATT
 GCTAAAGACTCTATGGACAGGGTATTTAAAAACTACCAAGACCCCTGACCATTATACTCTCC
 GGAAGATCAGCAGCCTGCCAATTCTCTTACCATCAAGAAGGACCTCCGGCTCTCAT
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACGCCAGATTCTGAGTCA
 CTTTGAAAAGCTGGAACCTCAGGCAGCAGTGTGAAGGCTTGGGGAACTAGACATTCTC
 TGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGTGCTGCTGCTAAGAATATTGAGGT
 CAAGAGCTCAGTCTCAATACCTGCAGAGGAGGCATGACCCAAACCCACCATCTTTACT
 GTACTAGTCTTGCTGGTCAGGTGTATCTTATTATGCAATTGCTTCTTGCTCATGAT
 TGCTTTATGCATCCCAATCTAATTGAGACCATACTGTATAAGATTTGTAATATCTT
 TCTGCTATTGGATATTTATTAGTTAATATTTATTATTTGGCTATTAATGTATTT
 ATTTTTTACTGGACATGAAACTTAAAAAAATTCAACAGATTATTTATAACCTGACTAG
 AGCAGGTGATGTATTTTATACAGTAAAAAAAAACCTTGAAATTCTAGAAGAGTGGCT
 AGGGGGGTATTCACTTGTATTCAACTAAGGACATATTACTCATGCTGATGCTCTGTGAGA
 TATTGAAATTGAACCAATGACTACTTAGGATGGGTTGGAATAAGTTGATGTGGAATT
 GCACATCTACCTTACAATTACTGACCACCCAGTAGACTCCCCAGTCCCATATTGTGTAT
 CTTCCAGCCAGGAATCCTACACGCCAGCATGTATTTCTACAAATAAGTTCTTGCTA
 CCAAAAAAAAAAAAAAAA

FIGURE 234

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLLWSPDPRPKMKASSLAFLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESIQLDTK PANRCCLLRHILLRLYLDdrvFKNYQTP
DHYTLRKISSLANSFLTICKDLRLSHAHMTCHC GEEAMKKYSQILSHFEKLEPQAAVVKALG
ELDILLQWMEETE
```

Important features of the protein:**Signal peptide:**

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGCCTACTGCTGA**ATG**TCCGCCGGAGGAGGAGGGCTTGCG
 CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCTACTGTCCGGCTGCGCGCTACCGTGGC
 CGAGCTAGCAACCTTCCCTGGATCTCACAAAAACTCGACTCCAAATGCAAGGAGAACAG
 CTCTTGCTCGGTTGGGAGACGGTGCAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
 GCCCTAGGGATCATTGAAGAGGAAGGCTTCTAAAGCTTGGCAAGGAGTGACACCCGCCAT
 TTACAGACACGTAGTGTATTCTGGAGGTGAAATGGTCACATATGAAACATCTCGAGAGGTTG
 TGTGGCAAAAGTGAAGATGAGCATTATCCCCTTGGAAATCAGTCATTGGAGGGATGATG
 GCTGGTGTATTGGCAGTTTAGCCAATCCAACGTGACTAGTGAAGGTTCAGATGCAAAT
 GGAAGGAAAAGGAAACTGGAAGGAAACCATTGCGATTTCTGGTGTACATCATGCATTG
 CAAAAATCTAGCTGAAGGAGGAATACGAGGGCTTGGCAGGTGGTACCCAATATAACAA
 AGAGCAGCAC**T**GGTAATGGGAGATTAAACCACTTATGATAACAGTGAACACTACTGGT
 ATTGAATAACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC
 TGTTAGCTCTATTCTGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCA
 CGAGATAAACAGGAAGGGACTTTGTATAAAATCATGACTGACTGCTGATTCAAGGCTGT
 TCAAGGTGAAGGATTCATGAGTCTATATAAGGCTTTACCATCTGGCTGAGAATGACCC
 CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
 TTT**TAA**

FIGURE 236

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGA
RESAPYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLCVVFGKSEDEH
YPLWKSVIDGMMAGVIGQFLANPTDLVKVQMQUEGKRKLEGKPLRFRGVHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP
ADVIKSRIQMNPDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF
```

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGCGCAGGGACGCCGGCAGGGTTGTGGCGACGAGTCCTCCCTGCAGCG
 GCCTGAAGTCGGCGTGGCGTTGAGGAAGCTGGATACAGCATTAAATGAAAATTTATGC
 TTAAGAAGTAAAAATGGCAGGCTCCTAGATAATTTCGTTGGCAGAATGTGAATGTATTG
 ACTGGAGTGAGAGAAGAAATGCTGTGCATCTGTTCTCGCAGGTATATTGTTTACAGGC
 TGGTGGATAATGATTGATGCAGCTGTGGTATCCTAACGCCAGAACAGTTGAACCAGCCT
 TCACACATGTGGTATTTCACATTGGCTTCTCATGATAAATGCTGTATCCAATGTC
 AGGTGAGAGGGTGTAGCTATGAAAGCGCTGTTAGGAAGAACAGGTGCTCGAGTTGGCTT
 TTCATTGGTTCATGTTGATGTTGGTCACTTATTGCTTCCATGTTGATTCTTTGGTGC
 ATATGTTACCCAAAATACTGATGTTATCCGGGACTAGCTGTGTTTCAAATGCACTTA
 TATTTTTAGCACTGTACAAATTGAGAACGAGAGCTATGGACCTTGAGATCAC
 TTCTTAAGTCACATTTCCTTGTATATTCTGTTGAGATAGGTTTTATCTCTCAGT
 ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTGTTCTTACATTATGTT
 TGAGTTTGAATAGTTTATGAAATTCTTATTTCATTGATAGACTGTTAATATGTA
 TATAATACAAGACTATATGAAATTGATAATGAGTATCAGTTTATTCTGAGATTAGAA
 CTTGATCTACTCCCTGAGGCCAGGGTACATCATCTGTCATTAGAAGTAACCACTTGT
 CTCTCTGGCTGGCACGGTGGCTCATGCCGTAAATCCAGCAGCTGGGAGGCCAGGG
 CCGATTGCTGAGGTCAGTGTTGAGACCCAGCCTGCCAACATGGCAAACCCATCTACT
 AAAAATACAAAATTAGCCAGGCATGGTGGTGGGTGCTGTAATCCAGCTACCTGGGAGGC
 TGAGGCAGGAGAACCGGGGGCAGAGGGTGCAGTGAGCTGAGTTGCGCCAC
 TGCACCTAGCCTGGGGAGAAAGTGAACACTCCCTCTCAAAAAAAAGACCACTCTCAGTATC
 TCTGATTCTGAAGATGACAAAAAAATATAGCTCATATATCTGGAATGAGCACTGAGCCA
 TAAAAGGTTTCAGCAAGTGTAACTTATTGGCCTAAAATGAGGTTTTTGGTAAAGA
 AAAAATATTGTTCTATGTTGAAAGAAGTGTACTTTATATAATGATTTTAAATGCC
 AAAGGACTAGTTGAAAGCTTCTTAAAAGAATTCTCTAATATGACTTTATGTGAGAA

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVAVGILFFTGGWWIMIDA VVYPKPEQLNHFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVPGLAVFFQNALI FSTLIYKFGRTEELWT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

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FIGURE 239

GTTGATGGCAAACCTCCTAAAGGAGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCA
 CTGGCGGCCCGCAACACTCCGTCTCACCTCTGGGCCACTGCATCTAGAGGAGGGCCGTCT
 GTGAGGCCACTACCCCTCAGCAACTGGGAGGTGGACTGTCAGAACGCTGGCCCAGGGTGGT
 GGTCAGCTGGGTAGGGACCTACGGCACCTGCTGGACACCTCGCCTTCTCCATCGAACAG
 GGAAGTGGGAGCCTGAGGCCCTGGGTGGAAGCTGACCCCCAACGCCACCCCTCACCTGGACAG
GATGAGAGTGTAGGTGCTCGCCTCTGGCCATCTTGCCATAGTCACGACATGGA
 TGTTTATTGAAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
 GCCTCGCCCCACCAAGGAGATCCAGGTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC
 AGCCAACTAACCTTGCGTTAAATCTCAGTGGGGCCAACGTCGTGGGCCACTATGTA
 GCTTTGAAGACCGCATGATCATGAGTCTGTGAAAACAATGTGGCAGAGGCCCTAACATC
 GCCCTGGTGAATGAAACCACGGAGCTGTGCTGGACAGAACGGATTGACATGTACTCTGG
 AGATGTTATGCACTAGTGAATTCTTAAAGAAATTCCGGGGGGTGCAGTGGTGTGGTGG
 CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAACACTCTCTGACTTG
 GGGAGTTCTACGCAAAACAACGGGCTCCGGACAGCTGGGTCTCATAGGAGCCAAGA
 CCTCAGGGGTAAAAGCCCCCTTGAGCAGTTCTTAAAGAACAGCCCCAGACACAAACAAATACG
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTAGGTGGC
 TGTGGCTCTCCTCAGCCAGGGCCTGAGAACGCTCTGCTGACTTAGGAGTCAGGCC
 GCAGGGCTGAGGAGGAGGAGCAGGGGGTGCCTGCGTGGAAAGGTGCTGCAGGTCTTGACGC
 TGTGTCGCCCTCTCCTCGGAAACAGAACCCCTCCACAGCACATCTACCCGAAGACC
 AGCCTCAGAGGGCTCTGGAACCAAGCTGCTGTGGAGAGAATGGGTGCTTCGTCAAGGG
 ACTGCTGACGGCTGGTCTGAGGAAGGACAAACTGCCAGACTTGAGCCAATTAAATTAA
 TTTTGCTGTTTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 240

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24963, pI: 9.64, NX(S/T): 1
MRVSGVLRLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPKPF
```

Important features:**Signal peptide:**

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGAGTTGTCTGGGAT
 CCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACA
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC
 TCACTCCTCCCTCCCTCTCTCTGCCTGCTTAGTCCTCTAGTCCTCAAATTCCCAGTCCC
 CTGCACCCCTCTGGGACACTATGTTGTTCTCCGCCCTCTGCTGGAGGTGATTGGATCC
 TGGCTGCAGATGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACATTGCCA
 GCCTCTTACCCCTGAGTGTGAAACAATGCCAGTCGCCCATCGATATTGACAGACAGTG
 GACATTGACCCCTGATTTGCCTGCTCGCAGCCCCACGGATATGACCAGCAGCTGGCACCGAGC
 CTTTGACCTGACAACAATGCCACACAGTGCAACTCTCTGCCCTCTACCTGTATCTG
 GGTGGACTTCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACAGGGTCAGAAAGGATC
 CCCAGGGGGTCAAAACACAGATCAACAGTGAAGCCACATTGAGGCTCCACATTGTAC
 ATTATGACTCTGATTCTATGACAGCTTGAGTGAGGTGCTGAGAGGCCTCAGGGCCTGGCT
 GTCCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
 TCACTTGATGAAAGTCAGGCATAAACAGTCAGAAGACCTCAGTGCCTCCCTCAACCTAACAGAG
 AGCTGCTCCCCAACAGCTGGGGCAGTACTCCGCTACAATGGCTCGCTCACAACTCCCCCT
 TGCTTACAGAGTGTGCTCTGGACAGTTTTATAGAAGGTCCAGATTCAATGAAACAGCT
 GGAAAAGCTCAGGGACATTGTTCTCACAGAAGAGGGCCCTCTAACGTTCTGGTACAGA
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGCTTTGCTCTTCATCCAAGCAGGA
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGAGGAATCTGGTTGGCTGTCTG
 CCTCTCCTGGCTGTTATTCTATTGCTAGAAAGATTGGAAGAAGAGGCTGGAAAACCGAA
 AGAGTGTGGCTTCACCTCAGCACAAAGCCACGACTGAGGCTAATTCTCTCAGATACCA
 TGGATGTGGATGACTTCCCTTCATGCCATCAGGAAGCCTCTAAATGGGGTGTAGGATCTG
 GCCAGAAACACTGTAGGAGTAGTAAAGCAGATGTCCTCCCTGGACATCTTAGAGAG
 GAATGGACCCAGGCTGTCAATTCCAGGAAGAACTGCAGAGCCTCAGCCTCTCAAACATGTA
 GGAGGAAATGAGGAAATCGCTGTGTTAATGCAGAGANCAAACCTGTTAGTTGAGGG
 GAAGTTGGGATATAACCCAAAGCTCTACCCCTCACTTTATGCCCTTCCCTAGATA
 TACTGCAGGGATCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTGATCAATA
 TATTGGAAATTAAAGTTCTGACTTT

FIGURE 242

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPDLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ
INSEATFAELHIVHYDSDSYDSLSEAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQFYRNGSLTPPCYQSVLWTVFYRRSQISMEQLEKLQGTL
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA
```

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 243

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQFPSLSLIPLTQM
LTLPDPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE
LPQI FTSLLIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTTPAGIQRSRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16

FIGURE 245

GGAGAGAGGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCCTGCCGCCCTCGGAGCGCGGGCG
 GAGCCAGACGCTGACCACGTTCTCTCCCTCGGTCTCCGCCCTCCAGCTCCGCCCTGCC
 GCAGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCCCTCCCCGCAGGGCTCGGCCCTCC
 TGCTGCTCCTGCTGCTGCAGCTGCCGCCGTGAGCGCTCTGAGATCCCCAAGGGGAAG
 CAAAAGGCGCAGCTCCGGAGAGGGAGGTGGACTGTATAATGGAATGTGCTTACAAGG
 GCCAGCAGGAGTGCCTGGTCAGAGCGGAGCCCTGGGCCAATGTTATCCGGTACACCTG
 GGATCCCAGGTGGGATGGATTCAAAGGAGAAAAGGGGAATGTCAGGGAAAGCTTGAG
 GAGTCCTGGACACCCAACTACAAGCACTGTTCATGGAGTTATTGAAATTATGGCATAGATCT
 TGGAAAATTCGGAGGTGTACATTACAAAGATCGTCAAAATAGTGCCTAAGAGTTTG
 TCACTGGCTACTCGGCTAAATGCAAGAACATGCTGTCAGCGTTGGTATTCACATT
 AATGGAGCTGAATGTCAGGACCTCTCCATTGAAGCTATAATTATTGGACCAAGGAAG
 CCCTGAATGAATTCAACAATTAAATTACATCGCACTCTCTGTGAGGACTTTGTGAAG
 GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTGGCATTGTCAGATTACCCAAA
 GGAGATGCTCTACTGGATGGAATTCAAGTTCTCGCATCATTATTGAAGAACATACAAATA
AATGCTTAAATTTCATTTGTCACCTCTTTTTATTATGCCTGGAAATGTTCACTTAAAT
 GACATTAAATAAGTTATGATACATCTGAATGAAAGCAAAGCTAAATATGTTACAGA
 CCAAAGTGTGATTCACACTGTTAAATCTACATTATTGCTTCATAGCACATTCTCAACCTA
 GGTTCAATATTTTTAGTGGTTAGAATACTTCTTCATAGTCACATTCTCAACCTA
 TAATTGGAAATTGTTGGTCTTTGTTCTTAGTATAGCATTAAAAAAATA
 TAAAAGCTACCAATCTTGACAAATTGTAAGAATTTTTATATCTGTTAAAT
 AAAAATTATTCACACA

FIGURE 246

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAAASPQRLLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRNSNALRVLFGSILRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMN
STINIHRRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217